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Abk69965
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Ada013706
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Ada01149
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Adb96913
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Add10331
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/product= "human secreted protein"
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ADE37518
ADD95289
ADE37989
ADE76078
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ADD88226
ADD90807
ADE51660
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ADB86916
ADB66071
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    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                  nucleic search, using frame_plus_p2n model
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                                                                                                                                                                3373863 seqs, 2124099041 residues
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ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn

651 GGTTACTGCTTCTTCAAGAACCAGAGAATTCCACGGACACCACCACCACCA

650 180

GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro

ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu

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This DNA encodes a human secreted protein. The specification provides secreted protein sequences (AAW63691 to AAW6369) encoded by the mucleic acid sequences shown in AAV43610. The invention provides a method of identifying a secreted polypeptide which is modified by rough microsomes. The secreted proteins can be used in assays to determine contrivities, such as cytokine, cell proliferation, or cellular differentiation activity, chemotactic or chemokinetic activity, nemostation activity, receptor/ligand activity, tumour inhibition, or thrombolytic activity, receptor/ligand activity, tumour inhibition, or canti-inflammatory activity. The proteins activity, tumour inhibition, or anti-inflammatory activity. The protein activity, tumour inhibition, or continuous activity in protein expression. They activity to complete the protein activity to in protein expression. They can be used in protein interaction assays, to identify ligands or binding proteins.

Compounds which affect the biological activities of the secreted proteins or their ability to interact with specific ligands can be identified using the proteins in screening assays. The proteins and antibodies that bind specifically to the protein can also be used to design diagnostic tests and therapeutic compositions for diseases which may be associated with altered expression of these proteins. Fusion proteins comprising, especially to transmembrane domains of the proteins can be contrained to there protein domains to cellular membrane or they can be associated contrained.
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                                                                                                                            Secreted human polypeptides - having cytokine, cell proliferation differentiation, activin or inhibin, tumour inhibition or anti-inflammatory activities.
        Kothakota
     Williams LT,
                                                                                                                                                                                                                          Claim 6; Page 31-32; 78pp; English.
  Garcia P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted extracellularly
                                                 WPI; 1998-348453/30.
P-PSDB; AAW63684.
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  Escobedo J,
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BP; 332 A; 450 C; 406 G; 317 T; 0 U; 0 Other; Sequence 1505

IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100 MetGluargarghisProvalcysSerGlyThrCysGluProThrGlnPheArgCysSer AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla AATGGCTGCTGCTGCAECGACAGTTTCCTGGAGTGTGACGACACCCCCCAACTGCCCCGAAGGCC SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArglleHis PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 351 TTCCCCAGGGACAAAGGGCACTGGGACCTGCCAACAACAAGAACTCTGCAAGGAGG CysTyrGlyAsnLysAsnAsnPheGluGluGluGluGlnCysLeuGluSerCysArgGly TGTTACGGCAACAACAACTTTGAGGAAGAGCAGCAGCTCGAGTCTTGTGCGGGC Arcceccordenacracaaccecrrcaeceaacacreececcecrrraecrareer IleSerLysLysAspValPheGlyLeuArgArgGluIleProlleProSerThrGlySer 0000 Length: Matches: Conservative: Mismatches: Indels: (1-1505)Gaps: US-09-935-390A-23 (1-206) x AAV43604 7.51e-115 1167.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: 21 231 43 61 81 411 471 121 101 Query Match DB: 셤 쉽 à δ g Š 원 원 슝 à ò g Š

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Sequence 1542 BP; 319 A; 507 C; 439 G; 277 T; 0

assay standards

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hepatocyte growth factor (HGF) activator (HGFA), which has a molecular weight of about 40 kD when determined by SDS-PAGE. The inhibitor, which was isolated from the human cancer cell line MKM45, can be used as an in vivo or in vitro regulatory factor for HGF or HGFA. It can also be used to raise antibodies, useful in kinetic studies of the inhibitor, or as
                                                                                                                                                                                                                                                                                                                     Inhibition, inhibitor, protease, hepatocyte, growth factor, activation, activator; human, cancer, cell line, MEM45, regulation, regulator, antibody, kinetic study, assay standard, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hepatocyte growth factor activator inhibitor and DNA - regulates hepatocyte growth factor and/or HGF activator in vivo or in vitro, and are used in kinetic studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes an inhibitor of the protease activity of
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                                                                                                                                                                                                                                                                 Hepatocyte growth factor activator inhibitor cDNA
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                                                                  AAT90038 standard; cDNA to mRNA; 1542 BP
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P-PSDB; AAW27368.
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                                                                              AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
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                                                       MetGluargarghisProvalCysSerGlyThrCysGlnProThrGlnPheArgCysSer
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This invention describes a preventive and/or treating agent for the diseases caused by the exasperation of activity of protease of plasma kallikrein, plasmin, unokinase and trypsin. The agent contains a protein, HAI-1 which has the following properties, M.W. of ca. 40,000 to 57,000 balton by SDS-PAGE and an activity of inhibiting protease activity of hepatocyte growth factor (HGP) activator. The HGP inhibiting activity of the protein is specific. HAI-1 shows a high inhibiting activity of plasmin, trypsin, HGF activator and plasma kallikrein but substantially no inhibiting activity on thrombin. This sequence encodes the human HAI-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1221
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                                                                                                                                                                                                                                                                                                                                                                                                                  A preventive and/or treating agent for the diseases caused by the exasperation of activity of protease - inhibits protease activity hepatocyte growth factor (HGP) activator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 6-8; 8pp; Japanese.
                                                                                                                                                                                                        97JP-00189480
                                                                                                                                                                                                                                                       97JP-00189480
                                                                                                                                                                                                                                                                                                   (MITU ) MITSUBISHI CHEM CORP.
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1167.00
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1. .105
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106. .1539
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Best Local Similarity:
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1041

981

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1101

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1161

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140

1. .1542 /*tag= a /product= "HAI-1"

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1401
1282 ATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGGAAATCCCCATTCCCAGGACAGGCTCT 1341
                                                                                                                                                                                                                                                                                                 ProThrProAlaSerSerThrValSerThrThrOluAspThrGluHisLeuValTyrAsn 200
                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; protease associated protein; HPRAP; cancer; inflammation; anti-HIV; antianaemic; antiarteriosclerotic; antiasthmatic; cytostatic; antiinflammatory; hepatotropic; antidiabetic; nephrotropic; antigout; antitinflammatory; hepatotropic; antidiabetic; nitudide; dermatological; antichrodid; immunosuppressive; thyromimetic; virudide; dermatological; neuroprotective; cardiant; osteopathic; antiarthitic; antiparasitic; antipsoriatic; uropathic; ophthalmological; antirheumatic; tranquiliser; vulnerary; antiulcer; immune disorder; gene therapy; HPRAP-2; gene; ds.
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                                                         ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu
                                                                                                                   1342 GrégaGarderes de de la construcció de la co
                                                                                                                                                                             GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro
                                                                                                                                                                                                                       Novel human protease associated proteins used for, e.g. the diagnosis prevention of cell proliferative and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protease associated protein HPRAP-2 coding sequence.
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134. .1180
/*tag= a
/product= "HPRAP-2"
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P-PSDB; AA017713.
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thrombocythaemia, AIDS, Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia, casthma, atherosclerosis, antonimue haemolytic ansemia, autoimmune the state of assase, atopic dernatitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dernatitis, dermatomyositis, diabetes mellitus, cappic dernatitis, dermatomyositis, diabetes mellitus, cappic dernatitis, dermatomyositis, diabetes mellitus, cappic dernatitis, dernational mithylogenes, erythema nodosum, atrophic gastritis, glomerulonephritis, conopositus, syndrome, gout, Grave's disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, conscentifizitis, osteoporosis, pancreatis, polymyositis, psoriasis, casteoarthritis, soleoporosis, pancreatis, polymyositis, psoriasis, castemic anaphylaxis, systemic lupus erythematosis, systemic sclerosis, thrombocytopenia, purpura, ulcerative colitis, uveitis, Werner syndrome, infections and trauma. The present sequence is the HPRAP-2 coding considering busined from the Derwent family equivalent US6171790
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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The present sequence is that of cDNA clone DNA35880-1160 (ATCC 209379)
encoding novel human immunomodulator protein PR0256 (UN0223) (see
encoding novel human immunomodulator protein PR0256 (UN0223) (see
chab20113). The clone was isolated from a human placenta cDNA library. The
predicted protein (58 kDa, pl 6.22) shows homology to human bikunin,
indicating protease inhibitor activity. The invention provides
comprising the proteins of the proteins of these
proteins or their agonists are useful for increasing infiltration of
inflammatory cells into a tissue of a mammal, stimulating or enhancing an
immune response in a mammal, or increasing the proliferation of T-
lymphocytes in a mammal, or increasing the proliferation of T-
lymphocytes in a mammal, or increasing the proliferation of T-
lymphocytes in a mammal in response to an antigen. Claimed compositions
comprising the PRO polypeptide or its antagonist have the opposite
effect. A claimed method for treating an immune related disorder, such as
a T cell disorder, involves administering the PRO polypeptide, an agonist
antibody or an antagonist antibody. The disorder is selected from
systemic lupus erythematosus, rheumatoda arthitis, osteoarthritis,
iuvenile chronic arthritis, spondyloarthropathy, systemic sclerosis,
dispathic inflammatory myopathy, Sjognen's syndrom, systemic
chrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
disease, demphatitis, primary biniary cirrhosis, graanlomatous
chromic active hepatitis, primary biniary cirrhosis, graanlomatous
hepatitis, inflammatory bowel disease (ulcerative
                                                                                                                                                      PRO256; UNQ223; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antisoriatic; antiathmatic; antiallergic; immunostimulant; protease inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pong S, Goddard A, Godowski PJ;
Mark MR, Marsters SA, Pitti RM, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO polypeptides, mucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
188. .1777
AAF30055 standard; cDNA; 2482 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 21; Fig 11; 127pp; English.
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                                                                                                                   Human cDNA encoding PR0256.
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188. .292
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293. .1774
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Wood WI;
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Watanabe CK,
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                                                                                                                                                                                                                                                                              Homo sapiens
                                                                             30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                      AAF30055;
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colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythem amultiforme and psoriasis), allergic diseases (such as sthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation diseases (such as graft rejection and graft-versus-host diseases) (all claimed). Claimed methods of diagnosting these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies and a method of stimulating the proliferation of T-lymphocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGluGlnCysLeuGluSerCysArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1457 TGTTATGGCAACAAGAAGAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1517 ATCTCCAAGAAGGAATGTGTTTGGCCTCAAGGCGGGAAATCCCCATTCCCAGCACAGGCTCT
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                                                                                                                                                                                                                                                            Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cacaccecedecere 1774
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                                                                                                                                                                                                                                                                                                                 Pred. No.; 3.94e-114
Score: 1163.00
Percent Similarity: 99.514
Best Local Similarity: 99.514
Query Match: 99.664
                                                                                                                                                                                                                      using PRO256
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The present invention relates to PR0256 or its agonist/antagonist may be used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, especially a human with cardiac hypertrophy, trauma, a type of tumour or age-related macular degeneration. PR0256 may be administered together with a cardiovascular endothelial, or angiogenic agent, a creation to the search inhibitory agent, or a cytocoxic agent. PR0256 may also be used to treat the disorders above, preferably through administration via ex vivo gene therapy. PR0256 or its agonist may be used to inhibit endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor, whereas an antagonist of PR0256 may be used to stimulate endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor. Stimulation or inhibition of the protease activity of a hepatocyte growth factor is preferably carried out where a mammal has a cardiovascular, endothelial, or renal injury or a restinosis disorder. The present sequence is human hepatocyte growth factor activator inhibitor, PR0256 cDNA
                                                                                                      Human, PRO256 protein, cardiovascular, endothelial, anglogenic disorder, cardiac hypertrophy, trauma, cardiant, age-related macular degeneration, gene therapy, anglogenesis, protease activity, hepatocyte growth factor, peripheral vascular disease, hepatic, renal injury, nephrotropic, tumour, restinosis, tranquillizer, vulnerary; cytostatic, hepatotropic, ss.
                                                                                                                                                                                                                                                                                           /ttag= a
/product= "Human hepatocyte growth factor activator
inhibitor, PRO256"
188. 292
/*tag= b
293. 1774
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/product= "Human mature hepatocyte growth factor
activator inhibitor, PRO256"
                                                                    Human hepatocyte growth factor activator inhibitor, PRO256 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated polypeptide designated PRO256 useful for treating a cardiovascular, endothelial, or anglogenic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney AL, Kirchhofer DK, Wood WI;
                                                                                                                                                                                                                                                   Location/Qualifiers
188. .1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 40; Fig 1; 124pp; English.
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28-NOV-2000; 2000US-0253665P.
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                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-541567/60.
P-PSDB; AAE09332.
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                                    19-NOV-2001
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AAD16721;
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Length: Matches: Conservative: Mismatches:

3.94e-114 1163.00 99.51%

> Percent Similarity: Best Local Similarity:

Alignment Scores:

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1336
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                                                                                                                                                                      1 MetGluhrgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, PRO, benign tumour; malignant tumour; lymphoid malignancy; leukaemia, neuronal disorder; stromal disorder; blastocoellc disorder; inflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; se.
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       Query Match:
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1157 AFGGAAAGGCGCCATCCAGTGTGCTCTGGCACCTGTCAGCCCACTTCCGCTGCAGC 1216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, and properties or anti-pRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagil, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy, ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PheProSerAsplysGlyHisCysValAspleuProAspThrGlyLeuCysLysGluSer 80
                                                                                                                                                                                                                                                                                                                                                                        Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
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                                                                                                                                                                                                                                                                        Hillan KJ;
                                                                                                                                                                                                                                                                                      Stone DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
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Smith V,
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                        å A, Godowski PJ,
Pitti RM, Roy MA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 50; Fig 11; 302pp; English.
            99US-0133459P.
99WC-US012252.
99US-0140653P.
99US-0144758P.
99US-0144758P.
99US-0145698P.
99US-0145698P.
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1163.00
99.51%
99.61%
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                                                                                                                                                                                                                                                                       Goddard A,
                                                                                                                                                                                                                                                                                     Pan J, P
Wood WI;
                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                       Ashkenazi AJ,
            11-MAY-1999;
02-JUN-1999;
22-JUN-1999;
                                                      22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
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Watanabe CK,
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                                                                                                             17-AUG-1999;
31-AUG-1999;
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1337 TTCCCCAGTGACAAAAGGGCACTGCGTGGACCTGCCAGACAGGACTCTGCAAGGAGAGC 1396

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1517 ATCTCCAAGAAGGATGTTTGGCCTGAGGCGGGAAATCCCCATTCCCAGGACAGGCTCT 1576
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                                                                                                                                                               GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro 180
CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnGlnCysLeuGluSerCysArgGly 120
                                                                                                           141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160
                                                                                                                                                                                                                       ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; attiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hyportrophy; atherosclerosis; hyportension; age-related macular degeneration; arterial restenosis; angina; rheumatodia tribritus; mycardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast cardinoma; liver cardinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
                                                     121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProlleProSerThrGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO256 cDNA sequence SEQ ID NO:41.
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02-AUG-2000; 2000US-0225595P.
17-AUG-2000; 2000US-0643557.
23-AUG-2000; 2000WO-US023352.
24-AUG-2000; 2000WO-US023328.
07-SEP-2000; 2000WS-0230978P.
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2000US-00665350
2000US-0242922P
2000US-0209238
2000WO-US030873
2000WO-US032678
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2001US-00767609.
2001US-00796498.
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18-SEP-2000; 2
24-OCT-2000; 2
08-NOV-2000; 2
10-NOV-2000; 2
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22-JAN-2001; 2
28-FEB-2001; 2
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1517 ATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGGAAATCCCCCATTCCCAGGACACGTTT
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               IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly
                                      CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnGlnCysLeuGluSerCysArgGly
                                                                                                                     1457 ferrardecaacaacaacaacrirreaggaagaacaacacacrecagrerrereagec
                                                                                                                                                        IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 88; gene; PRO; secreted protein; transmembrane protein; genetic disorder; tumour; cancer.
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22-SEP-2000; 200UUS-0230621P.
22-SEP-2000; 200UUS-02356147P.
10-NOV-2000; 200UUS-0235147P.
12-JAN-2001; 200UUS-0261910P.
16-JAN-2001; 200UUS-0261910P.
16-JAN-2001; 200UUS-0261910P.
16-JAN-2001; 200UUS-026493P.
25-FEB-2001; 200UUS-026431P.
25-FEB-2001; 200UUS-026431P.
26-FEB-2001; 200UUS-026431P.
28-FEB-2001; 200UUS-026431P.
28-FEB-2001; 200UUS-026439P.
28-FEB-2001; 200UUS-026439P.
28-FEB-2001; 200UUS-0274399P.
28-AFR-2001; 200UUS-022199P.
28-AFR-2001; 200UUS-0222199P.
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2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
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01-JUN-2001;
20-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1217 AATGGCTGCTGCATCGACAGTTTCCTGGAGTGTGACGACGCCCCAACTGCCCCGACGCC 1276
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                                                                                                                                                                                                                                                                                                          Baker KP, Ferrara N, Gerber H, Gerritsen MB, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                  One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 41; 565pp; English
28-FEB-2001, 2001WO-USG06520.
09-MAR-2001, 2001WO-USG0666.
14-MAR-2001, 2001US-00802706.
14-MAR-2001, 2001US-00802016.
22-MAR-2001, 2001US-00816744.
10-MAY-2001, 2001US-00854208.
10-MAY-2001, 2001US-00854208.
25-MAY-2001, 2001US-00866034.
25-MAY-2001, 2001US-00866034.
25-MAY-2001, 2001US-00866034.
30-MAY-2001, 2001WO-USG17092.
30-MAY-2001, 2001WO-USG17092.
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1163.00
99.51$
99.66$
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Best Local Similarity:
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This invention relates to the cDNA and protein sequences of novel
secreted and transmembrane polypeptides PRO polypeptides. The invention
comprises a tethod for producing the proteins of the invention by
recombinant means and antibodies specific for the protein of the
invention. The antibody may be used for detecting the PRO proteins of the
invention and may be used to modify their activity. Polymuclectides may
be used as hybridisation probes for a cDNA library to isolate the full-
compress for mapping the gene which encodes that PRO and for genetic
analysis of individuals with genetic disorders, in assays to identify
other proteins or molecules involved in binding reaction, to generate
the proteins or molecules involved in binding reaction, to generate
the charmans or knock-out animals which in turn are useful in the
development and screening of therapeutically useful reagents, for
chromosome identification, and tiseum typing. The PRO polypeptides are
electrophoresis purposes. The sequences may also be used to detect
overexpression on PRO polypeptides in cancerous tumours and for screening
for differentially expressed genes using microarray technology. The
invention
                                                                                                                                                                        New PRO polypeptides and polynucleotides encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or genetic analysis of individuals with genetic disorders.
                              Grimaldi JC;
Wood WI, Zhang Z;
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                           E, Goddard A,
Watanabe CK,
                           Filvaroff E
Stephan J,
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                         Eaton DL,
Smith V,
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                                              Gurney AL,
Fong S;
                         Baker KP
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1157 AIGGAAAGGCGCCAICCAGIGCFGCTGGGACCTGICAGCCCACCCAGTICCGCTGCAGC 1216
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Mismatches:
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Alignment Scores:
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1517 ATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCCACAGGCTCT 1576
                            160
                                                                      GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
                                                                                                                      ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
                                                                                                                                                                                                                                                                                                                                           Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atheroscalerosis; cardiac hypertrophy; gene therapy; endochelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
                                                                                        1637 GGTTACTGCTTCTTCAAGAACCAGAGAAAGGACTTCCACGACCACCACCACCACCACCA
                        141 ValGluMetAlaValAlaValPheLeuValIleCyBIleValValValAlaIleLeu
                                                                                                                                                                                                                                                                                                                     Human angiogenesis related cDNA PRO256 SEQ ID NO: 41.
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23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WG-US023938.
18-SEP-2000; 2000US-023938.
18-SEP-2000; 2000US-00665350.
24-OCT-2000; 2000US-0065932P.
08-NOV-2000; 2000WG-0303938.
10-NOV-2000; 2000WO-US039673.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WG-US032678.
20-DEC-2000; 2000WG-US034678.
21-DEC-2000; 2000WG-US03678.
22-DEC-2000; 2000WG-US034678.
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2001US-00802706.
2001US-00808689.
2001US-00816744.
2001US-00828366.
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2001US-00796498.
2001WO-US006520.
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22-MAR-2001; 2001
05-APR-2001; 2001
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09-MAR-2001;
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25-MAY-2001;
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161 GlyTyrCysPhePhelygasnGlnargLysAspPheHisGlyHisHisHisHisProPro 180 [[[[[[]]]]]]]]]
1637 GGTTACTGCTTCTTCAAGAACCAGAGAAAGGACTTCCACGACACCACCACCACCACCACCA 1696
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                                                                                                                                            1397 ATCCCGCCTGGTACTACAACCCCTTCAGCGAACACTGCGCCCCCTTTACCTATGGTGGT 1456
                                                                                                                    IleSerLyslysAspValPheGlyLeuArgArgGluileProlleProSerThrGlySer 140
                                                                                                                                                                                               141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160
                                      CysTyrGlyAsnLysAsnAsnPheGluGluGluGluGlnCysLeuGluSerCysArgGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TWF-alpha; blood; chondrocyte cell; tumour; adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer; microvascular endothelial cell; endothelial cell tube formation; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, and PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grimaldi JC;
Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Filvaroff E, Goddard A,
Stephan JP, Watanabe CK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          HisThrThrArgProLeu 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 9; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA01277 standard; cDNA; 2482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-2001; 2001US-0290589P.
29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO polymucleotide #5.
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Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-625484/59.
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Fong S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1337 TICCCCAGIGACAAAGGGCACTGCGIGGACCTGCCAGACACAGACATCTGCAAGAAGAGAGC 1396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thromopolhebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGluArgIleHis
                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1, Fig 41, 567pp; English.
30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
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1163.00
99.51%
99.51%
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(GIRM) GURNEY A L.
(HILL) HILLAN K J.
(PANA) PAN J.
(PANA) PAN J.
(PANA) PAN J.
(STEP) STEPHAN J F.
(WILL) WILLIAMS P M.
(WILL) WOOD W I.
                                                                                                                                       GERBIR H.
GERRITSEN M E.
GODDARD A.
                                                                               GENENTECH INC.
BAKER K P.
FERRARA N.
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                                                                               (GETH )
(BAKE/)
(FERR/)
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invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TYP-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for colon, breast, prostate, rectal, cervical and liver tumours). The detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as antisense RNA and DNR and in gene therapy. The polymucleotides may also antisense RNA and DNR and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful cuseful in the development and screening of therapeutically useful casedents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cells cut the formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a known of the the the invention represents a human PRO polynucleotide of the invention.

Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

1277 TCCGAGGCTGCCTGTGAAAATACACGAGTGGCTTTGACGAGTGCCGCGTCCAT 1336 1337 TTCCCCAGTGACAAAGGGCACTGCGTGGACCTGCCAGACACACAGACTCTGCAAGAGAGC 1396 ValGluMetAlaValAlaValPheLeuVallleCysIleValValValValAlalleLeu 160 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200 1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysFroAspAla SerAspGluhlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGluArgIleHis PheProSerAspLysGlyHisGyeValAspLeuProAspThrGlyLeuCysLysGluSer 81 IleProArgTrpTyzTyzAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 1397 ATCCGGGGTGGTACTACAACCCTTCAGCGAACACTGGGCCCGGTTTACCTATGGTGGT 1457 TGTTATOGCAACAAGAACAACTTTGAGGAAGAGCAGTGCCTGGAGTCTTGTGGGGC IleSerLysLysAspValPheGlyLeuArgArgGluileProlleProSerThrGlySer GlyTyrCysPhePheLysAsnGlnArqLysAspPheHisGlyHisHisHisHisProPro CysTyrGlyAsnLysAsnAsnPheGluGluGluGluGlnGluGerCysArgGly 1517 ATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCT 0 - 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-935-390A-23 (1-206) x ADA01277 (1-2482) Gaps: 3.94e-114 1163.00 99.51% 99.51% Similarity: Percent Similarity: Best Local Similarit Query Match: gnment Scores: 1157 21 61 43 121 1577 101 141 161 181 B. ò ద ਨੇ ò 유 ò 뎚 ò g ò a 8 S S ઠે g õ g 셤 ò

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HisThrThrArgProLeu 206

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Grimaldi JC;
Wood WI, Zhang Z;
                                                                                                sa; gene; human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.
                                                                                 Human cDNA encoding secreted/transmembrane polypeptide PRO256.
                                                                                                                                                                                                                                              Goddard A,
Watanabe CK,
                                                                                                                                                                                                                                              Baton DL, Filvaroff E,
Smith V, Stephan JP,
1757 CACACCACCGGCCCCTC 1774
                                     ADA43706 standard; cDNA; 2482
                                                                                                                                                                                                        29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
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                                                                 20-NOV-2003 (first entry)
                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                           US2003064474-A1.
                                                                                                                                            Homo sapiens.
                                                                                                                                                                           03-APR-2003.
                                                                                                                                                                                                                                                     Gurney AL,
Fong S;
                                                    ADA43706;
                                                                                                                                                                                                                                              Baker KP,
                      RESULT 12
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New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 PRO21383, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.

2003-605867/57. P-PSDB; ADA43707.

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or in

Claim 2; Fig 9; 308pp; English.

The invention relates to an isolated secreted/transmembrane (PRO)

C polypeptide, having at least 80% sequence identity to a sequence selected

from any one of the 57 amino acid sequences given in specification, or to

a sequence encoded by a nucleic acid molecule selected from any one of

the nucleic acids deposited under any of the ArC accession numbers given

C action specification, or a sequence having at least 80% identity to PRO

c lacking its associated signal peptide. Also included are vectors,

transformed host cells, anti-PRO antibodies, the nucleic acids encoding

PRO, PRO fusion proteins, inducing endothelial cell tube formation (by

administering PRO281, PRO360, PRO489, PRO499, PRO6308, PRO6000,

CC administering PRO281, PRO3093 or PRO34274 polypeptide or its agonist) and

CC an oligonucleotide probe derived from any one of the above mucleotide

Sequences. PRO6018 polypeptide is useful for stimulating the

proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080

CC and PRO21383 polypeptides are useful for stimulating the proliferation of

microvascular endothelial cells. PRO6011, PRO4487 and PRO6006

CC and PRO21383 polypeptides are useful for stimulating the proliferation of

microvascular endothelial cells. PRO6011, PRO4487 and PRO6006

CC polypeptides are useful for inhibiting the proliferation of human

CC detecting the presence of tumour in a mammal, including tumours of lung,

CC colon, breast, prostate, rectal, kidney and liver. PRO231, PRO1560,

CRO1019, PRO4499, PRO6309, PRO6000, PRO10275, PRO22031 and

CRO1019, PRO4499, PRO6309, PRO600, PRO10275, PRO22031 and

CRO1024274 polypeptides are useful for inducing endothelial cell tube

CC formation. PRO or the antibody are useful in the preparation of a

CC microvate probes are useful for inducing endothelial cell tube

CC formation. PRO or the antibody are useful in the preparation of a

CC microvate probes are useful for inducing endothelial cell as a

CC microvated gene, and as antisense probes. PRO 01990 profice sequences,

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1217 AATGGCTGCTGCTGCATCGACAGTTTCCTGGAGTGTGACGACACCCCCAACTGCCCCGACGCC 1276
                                                                                                                                                                                                                                                                    1337 TTCCCCAGTGACAAAGGGCACTGCGTGGACCTGCCAGACACACAGCAAGGAAGAGC 1396
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                                                                                                                                                                                 MetGluArghrgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
                                                                                                                                                                                                                           AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
                                                                                                                                                                                                                                                                                                                   80
hybridisation probe, in chromosome and gene mapping, in the generation antisense RNA and DNA, and for the preparation PRO polypeptides. PRO an PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence encodes a PRO protein.
                                                                                                                                                                                                                                                                                                             PheProSerAsplySGlyHisCysValAspLeuProAspThrGlyLeuCysLySGluSer
                                                                                                                                                                                                                                                                                                                                                        IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly
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                                                     BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
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Matches:
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Mismatches:
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The invention relates to an isolated secretedy transmemorane (**rw) or the invention relates to an isolated sequence identity to a sequence selected from any one of from any one of the 57 animo acid sequences given in specification, or to a sequence encoded by a mucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCT accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO islon proteins, inducing endothelial cell tube formation (by RMO islon proteins, inducing endothelial cell tube formation (by RMO islon proteins), inducing endothelial cell tube formation (by RMO islon). PRO 18039, PRO 180499, PRO 1803, PRO 18039, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or PRO21383 useful for stimulating the proliferation or differentiation of chondrocyte cells and detecting the presence of a tumor in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                          Grimaldi JC;
Wood WI, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated secreted/transmembrane (PRO)
microvascular endothelial cell; tumour; lung tumour; colon tubeast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.
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Stephan JP, Watanabe CK,
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18-JUL-2002; 2002US-00197942.
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Smith V,
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                                                                                         Homo sapiens.
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Fong S;
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Length: Matches: Conservative: Mismatches: Indels: Gaps:

3.94e-114 1163.00 99.51% 99.51% 99.66%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

Score:

us-09-935-390a-23.rng

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1217 AATGGCTGCTGCACGACAGTTTCCTGGAGTGTGACGACGCCCCGAACTGCCCCCGACGCC 1276
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                                                                              21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla 40
                                                                                                                                                                                      PheProSerAsplySGlyHisCysValAspleuProAspThrGlyLeuCysLysGluSer 80
US-09-935-390A-23 (1-206) x ADA43474 (1-2482)
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29-OCT-1999;
02-DEC-1999;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The truvention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for proliferation or differentiation of chondrocyte cells and a method for proliferate, rectal, kidney and liver tumours). The polymucleotides are useful in molecular biology, including uses as bybridisation probes, in chromosome and gene mapping, in generating antiense RNA and bNA and in generating the presence of the polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the classification for an expensive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such a survey. For stimulating and inhibiting proliferation of human microvascular endothelial cells and for inducing endothelial cell tube for summans.
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                                                                                   Grimaldi JC;
Wood WI, Zhang Z;
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Conservative:
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Indels:
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                                                                                   Filvaroff E,
Stephan JP,
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29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
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Smith V,
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Best Local Similarity:
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                                                                                   Baker KP, E
Gurney AL,
Fong S;
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Pred. No.:
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1457 TGTTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGC 1516
                                                               121 IleSerLysLysAspValPheGlyLeuArgArgGlulleProlleProSerThrGlySer 140
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Wood WI, Zhang Z;
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Watanabe CK,
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Smith V, Stephan JP,
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29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
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transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO-PRO inductions inducing endothelial cell tube formation (by administering PRO281, PRO180, PRO180, PRO499, PRO6800, PRO6800, PRO180, PRO180, PRO180, PRO6800, PRO6800, PRO18018, PRO281207, PRO28933 or PRO180, PRO6800, PRO6800, PRO18018, PRO28018, PRO28
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1637 GGTTACTGCTTCTTCAAGAACCAGAGAATGCATTCCACGGACACCACCACCACCACCA 1696

161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180

1577 gredadarederereacarerrecregrearerecarreregregregregredecarerre 1636

141 ValGlumetalaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu

1517 Arcrecaagaaggargrerriggeergaggeggaaarceeearreeageacrer 1576

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Search completed: April 22, 2004, 08:29:56 Job time : 401 secs

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-MODEL=frame+ p2n.model -DEV=xlh
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-UNITS=bits -STRAT=1 -END=-1 -MATRIX=rge -MINNATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -TR_MIN=15 -MAXLEN=2000000000
-USER=-USO935390 @CGN 1 1 3731 @runat 20042004 144849 10383 -NCFU=6 -ICPU=3
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-DBV TIMEOUT=120 -WARN TIMEOUT=30 -TREMENS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                    April 22, 2004, 07:00:24; Search time 3729 Seconds (without alignments) 2394.386 Million cell updates/sec
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                  OM protein - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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| SUMMARIES | ID | | ^ 6 | 9 0 | R21838 | 444 | 2 | 00 | AR123705 | 50 | 4 | 60 | | AY296715 | 8 | AX201332 | AX211596 | AX454456 | AX490934 | AX574482 | AY358969 | BC005769 | BC053341 | AF099018 | AC025166 | AC012476 | BD241927 | AR237110 | AR260603 | AR278134 | AR366830 | AR370726 | AR392231 | AR399866 | AR405133 | AX106233 | AX140524 | AX200384 | AX267040 | φ | 5732 | 32 | AR237133 | 10 | 7815 | AR366853 |
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                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1542)
Shimomura, T., Kawaguchi, T., Kitamura, N. and Miyazawa, K.
Protein, DNA coding for same and method of producing the protein
Patent: US 6225081-A 8 01-MAY-2001;
Location/Qualifiers
1. 1542
                         161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisFroPro
                                                                                    1 MetGluArgArgHisProValCysSerGiyThrCysGlnProThrGlnPheArgCysSer
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ARI48260
ARI48260.1 GI:15112350
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                         TON Secreted human proteins. 1505 bp DNA linear PAT 27-AUG-2002 BD063229 | 161.22608832 | 160.3229 | 161.22608832 | 161.22608832 | 161.22608832 | 161.22608832 | 161.22608832 | 162.2608832 | 162.2608832 | 162.2608832 | 162.2608832 | 162.2608832 | 162.2608832 | 162.260832 | 162.260832 | 162.260832 | 162.260832 | 162.260832 | 162.260832 | 162.260832 | 162.260832 | 162.260832 | 162.2622 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2632 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623 | 162.2623
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Conservative:
Mismatches:
Indels:
Gaps:
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Topology: Linear,
Key
Location/Qualifiers
                      NA

    1505
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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                                                                                                                                                                                                                                                                                                                                                                                                                           101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGlnGlnCysLeuGluSerCysArgGly 120
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                             21 AsnGlyCysCysIleAspSerPheleuGluCysAspAspThrProAsnCysProAspAla 40
                                                                                                                           41 SerAspGluAlaAlaCySGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis 60
                                                                                                                                                                                                                            61 PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer 80
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Preventive and/or remedy for diseases caused by protease activity
E21838
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases I to 1542)

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A61K37/547
Strandedness: Double;
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Patent: JP 199035480-A 1 09-FEB-1999;
MITSUBISHI CHEM CORP
OS Homo sapiens
PN JP 199935480-A/1
D 9-FEB-1999 D PF 1997189480
PR TOSHIYA KAWAGUCHI
PC A61KZ8/22 A61KZ8/00, A61KZ8/80
PC A61KZ8/22 A61KZ8/00, A61KZ3/64
PC A61KZ7/54, A61KZ7/02, A61KZ7/64
PC Strandedness: Double;
CC Topology: Linear;
FH Key
CDS
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JP 1999035480-A/1.
Homo sapiens (human)
Homo sapiens
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Human cDNA encoding HAI-I, an inhibitor of HGF activator.
E12898
                                             1462 CCCACCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1521
1342 GTGGAGATGGCTGTCGCAGTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATCTTG 1401
                                                                                                                                              181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
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1 (Joases 1 to 1542)
Shimomura, T., Kawaguchi, T., Kitamura, N. and Miyazawa, K.
NSW PROTEIN, DNA CODING THE SAME AND PRODUCTION OF THE PROTEIN PATENT: JP 1997095497-A 1 08-APR-1997;
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PR 24-JUL-1995 JP 95P 187135
PI SHIMOMURA TAKESHI, KAWAGUCHI TOSHIYA, KITAMURA NAOMI, PI
MIYAZAWA KELJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product = 'HAI-I precursor'
peptide 1.05
peptide 106..1539
/product = 'HAI-I'.
Location/Qualifiers
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/organism='Homo mapiens'
/cell_line='MKN45'
1. .1542
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Key Location/Qualifiers
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/db_xref="taxon:9606"
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JP 1997095497-A/1
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BT007425.
BT007425.1 GI:30583688
FLI_CDNA.
Homo sapiens (human)
                                                                                                                  4.72e-117
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peptide 1..105
Location/Qualifiers
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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8 from patent US 6465622.
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Seguence 8 from patent 1
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AR237449.1 GI:27282185
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1 (bases 1 to 1542)
Shimomura,T., Kawaguchi,T., Kitamura,N. and
Protein, DNA coding for same and method of
Patent: US 6465622-A 8 15-0CT-2002;
Location/Qualifiers
.u.1542
/organism="unknown"
/mol_type="mRNA"
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Matches:
Conservative:
Mismatches:
Indels:
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Synthetic construct

synthetic construct

artificial sequences.

CE I (bases 1 to 1542)

RS Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,

Direct Submission

AL Submitted (17-JUL-2003) BD Biosciences Clontech, 1020 East Meadow

circle, Palo Alto, California 94303, USA

CE (bases 1 to 1542)

R Kannine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,

Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,

Elelan,M. and Farmer,A.

Direct Submission

AL Submitted (12-JUL-2003) BD Biosciences Clontech, 1020 East Meadow

circle, Palo Alto, California 94303, USA

This CDS clone is a part of a collection of human full length

circle, Palo Alto, California 94303, USA

This CDS clone is a part of a collection of human full length

circle, Palo Alto, California 94303, USA

This CDS clone is a part of a collection of human full length

Harvard Institute of Proteomics. Each CDS has been cloned in two

forms: with and without stop-codon (to allow fusion with C-terminal

tag). The CDS has been directionally cloned und the clone: 'ACC' after

sylvasion between the Sall and Hindill sites of the

pDNR-DUM. vector. Additional sequences in the clone: 'ACC' after

Sall site and before MTG' to provide Kozak consensus sequence;
'GG' after last codon and before Hindill site to maintain reading

frame. Clone distribution: http://bloinfo.clontech.com/orfclones.

1. 1542

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This CDS clone is a part of a collection of human full length

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This CDS clone is a part of a collection of human full length

This CDS clone is a part of a collection of human full length

Harvard institute of Proteomics. Each CDS has been cloned in two

forms: with and without stop-codon (to allow fusion with C-terminal

tag). The CDS has been directionally cloned using BD In-Fusion (TM)

cloning system between the Sall and HindIII sites of the pDRR-DUAL

vector. Additional sequences in the clone: 'ACC' after Sall site

and before 'ATC' to provide Kozak consensus sequence; 'GG' after

last codon and before HindIII site to maintain reading frame.

Clone distribution: http://bioinfo.clontech.com/orfclones.
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1542)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Bisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Parmer, A. Cloning of human full-length CDSs in BD Creator (TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
2 (bases 1 to 1542)
2 (bases 2 to 1542)
3 (Alaine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Kondinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
Direct Submission
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LEQPROSEDA TAACFILNCLYBGNFVCKRAPREGFINTLITREVYRSYRGLKTGGFGGS
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LFQLIVYSSDHPEDDIANTVTVLSTKGTFDYCLASNKVGRCRGSFPRWYDPTEQICY
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FLECDDTPNCPDASDEAACEKYTSGFDELQRIHPPSDKGHCVDLPDTGLCKESIPRNY
YNPFSEHCARFYYGGCYGNKANFREEBQCLESCRGISKGUVYVFGLRREIPIPSTGSVEM
AVAVELVICIVVVVAILGYCFFKNQRKDFHGHHHPPPTPASSTVSTTEDTEHLVYNH
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/note="Vector: pDNR-Dual"
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/clone=lib="BD Creator(TM) CDS Library derived from MGC

collection:

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Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Colling, P.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Malleh, S.S., Gasak, S.A., McEwan, P.J., Malek, J.A., Gunatane, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Mazny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Young, A.C., Shevchenko, Y., Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodrigues, R.C., Grimwood, J., Schevchenko, Y., Butterfield, Y.S., Kazywinsk, M. J., Shalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Manner, A., Manner, J.W., S., Kazywinsk, M. J., Schein, J. 
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Submitted (01-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Strausberg, R.
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PN JP 2002513572-A/2
PN JP 2002513572-A/2
PP 28-APR-1999 UP 2000547229
PP 01-MAY-1999 US 09/071709
PI DENNIPER L HILLMAN, TOM Y TANG, PREETI LAL, NEIL C CORLEY, KARL J GUEGLER,
PI CHANDRA PATTERSON
PC C121N15/09, A61K38/00, A61K45/00, A61P19/02, A61P35/00, A61P37/02,
PC C07K16/38, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02 PC C07K16/38, C12N15/00
PC C07K16/38, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02 PC A61K37/02, C12N5/00
PC A61K37/02, C12N5/00
PC Lncyte clone 1319265
FH Key Location/Qualifiers
FT Source (human)'.
                                         1100 CCCACCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAAC 1159
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28-APR-1999 JP 2000547229
01-MAY-1998 US 09/071709
JENNIFER L HILLMAN, TOM Y TANG, PREETI LAL, WEIL C CORLEY, KARL J
                ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
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Mammalla, Butheria, Primates, Catarrhini, Hominidae, Hono.
1 (bases 1 to 1870)
Hillman,J.L., Tang,T.Y., Lal,P., Corley,N.C., Guegler,K.J. and
Patterson,C.
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Patent: JP 2002113572-A 2 14-MAY-2002;
INCYTE PHARMACUTICALS INC
OS Homo sapiens (human)
PN JP 2002513572-A/2
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HOMO Sapiens (human)
HOMO sapiens
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/organism="Homo sapiens"
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ABUUUUUS 104-MAR-1998 DP MRNA linear PRI 04-MAR-1998 Homo sapiens mRNA for hepatocyte growth factor activator inhibitor, complete cds.
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                                                                                                       GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisBroPro 180
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Submitted (24-DBC-1996) Kimitoshi Denda, Tokyo Institute of
Submitted (24-DBC-1996) Kimitoshi Denda, 4259 Nagatsuta, Midori-ku,
Technology, Department of Life Science, 4259 Nagatsuta, Midori-ku,
Yokohama, Kanagawa 221, Japan (B-mail:kdenda@bio.titech.ac.jp,
Tel:45-924-5702, Fax:45-924-5771)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Eomo.
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                          1214 ATCCCGCGCTGGTACTACAACCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                      CysfyrGlyaniyaAsnAsnPheGluGluGluGlnGlnCysLeuGluSerCysArgGly
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          1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer
                                                                                  21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla
                                                                                                                                                           SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis
                                                                                                                                                                                                Phe ProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer
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hepatocyte growth factor activator inhibitor.
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Denda, K.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gl: 4504328.

Location/Qualifiers
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FLCODDFWOFDASDBAACEKTYSGPSELQR IHFPSDKGGTCVDLEPTGCKES IPRWY
YNPFSEHCARFYYGGCYGNKNNFEEGQCLSCRGISKGVYFGLREIF I FSTGSVEM
AVAVPLYICIVVVVALIGYCPPKNQRKOFHGHHHPPPTPASSTVSTTEDTEHLVYNH
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/codon start=1
/products start=1
/products precursor"
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1175. .1330
/hote="KU; Region: BPTI/Kunitz family of serine protease inhibitors"
/db_xref="CDD:smart00131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         794. .955
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inhibitors"
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                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanGsystemsbiology.org
Anup Madan, Jessica Fahbey, Brin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db_xref="LocusID:6692"
/db_xref="MIM:605123"
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1004. .1117
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Strausberg, R.L., 2486)

Strausberg, R.L., Peingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Colline, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhar, N.K., Hopkins, R.F., Zeeberg, B., Buetow, K.H., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Carninci, P., Prange, C., Raha, S.S., McEwan, P.J., McKernan, K.J., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Norley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Willalon, D.K., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Hulyk, S.W., Villalon, D.K., Mullahy, S.J., Gungrane, P.J., Lu, X., Gibbs, R.A., Sahey, J. Halton, B., Garcia, A.M., Gay, L.J., Lu, X., Gibbs, R.A., Sanchaz, A., Whiting, M., Madan, A., Youchan, J.W., Green, S.D., Dickson, M.C., Ratteman, M., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanchaza, M., Schein, J.B., Jones, S.J. and Marra, M.A., Proc. Natl. Acad. Sci. U.S., 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 22 Row: h Column: 7. Location/Qualifiers
                                                                                                                              BC018702 2486 bp mRNA linear PRI 12-NOV-2003 Homo sapiens serine protease inhibitor, Kunitz type 1, transcript variant 2, mRNA (cDNA clone MGC:15571 IMAGE:3140292), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Steven Jones, Jennifer Asano, Ian Bosdet, Frin Garland, Ran Guin, Susanna Chai, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Fawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R. Direct Submission of Direct Submission (NGC). National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help deak
Manil: gapba-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The 1.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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                                                                                                                                                                                                                           BC018702
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                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                BC018702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GlytyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisProPro 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ProthrProAlaSerSerThrValSerThrThrGluAsoThrGluHisLeuValTyrAsn 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArglleHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PhebroSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1397 TGTTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTGGAGTCTTGTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer
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206
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Conservative:
Mismatches:
Indels:
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176_.1717
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 2270;
Kirchhofer, D.; Peek, M., Li, M., Stamos, J., Eigenbrot, C.,
Kadkhodayan, S., Eliott, J.M., Corpuz, R.T., Lazarus, R.A. and Moran, P.
Tissue-expression, protease-specificity and Kunitz domain functions of HAL-1B, a new splice variant of hepatocyte growth factor unhibitor-1 (Daybulished 2370)
Yuan, J. and Moran, P.
                                                                                                                                                                                                                                  AY296715 2370 bp mRNA linear PRI 01-JUN-2003 Homo sapiens hepatocyte growth factor activator inhibitor 1B (HAI1) mRNA, complete cds.
                                                                                                                                                                                    1538 GIGGAGAIGGCOGTGCTCCTGCTCATCTGCATTGTGGTGGTGGTAGCCATCTTG 1597
                                                                                                                                                             GlyTyrCysPhePheLyBAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genentech Inc, One DNA Way
               121 ileSeriysiysAspValPheGlyLeuArgArgGlulleProlleProSerThrGlySer
                                   1478 ATCTCCAAGAAGGATGTGTTTGGCCTGAGGGGGGAAATCCCCATTCCCAGCACGCTCT
                                                                                     141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValValBlaIleLeu
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Homo sapiens
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Pred. No.:
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PAGADCLNS FTAGVPGFVLDTVAS VSNGATFLES PFTRRGMCVRACCTTONCNIALV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCCCAGTGACAAAGGGCACTGCGTGGACCTGCCAGACACACGACTCTGCAAGAGAGA 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 CysTyrGlyAsnLysAsnAsnPheGluGluGluGluGlnGlnCysLeuGluSerCysArgGly 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheProSerAspLysGlyHisCy8ValAspLeuProAspThrGlyLeuCysLysGluSer 80
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inhibitors"
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clone <u>lib="NIH MGC 21"</u>
lab host="DH10B-R"
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2000
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6000
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                         gene="SPINT1"

"note="Bynonyms: HAI1, HAI"

'db_xref="LocusID:6692"

'db_xref="MIM:605123"

197. .1738
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/db_xref="CDD:cd00109"
1148. .1261
                                                         'note="Vector: pOTB7"
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1167.00
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| /Organism="Homo sapiens" /db_xref="taxon:9606" /db_xref="taxon:960 | 1157 ATGGAAAGGCGCGATCTGGCACCTGCACCCCACCCCCACCTCCCCCCCC | KEYNORDS SOURCE Homo sapiens ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V., |
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| Score Similarity 99.51% Conservative 0 | 1177 TCCGGGGGGGGGGGGACCGGAAGAGGGGGGGGGGGGGGG | 1,R ate |

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                                                                                                                                                                                                                                                                                                                       PheProSerAsplysClyHisCysValAspLeuProAspThrGlyLeuCysLysCluSer 80
                                                                                                                                                                                                                                                                                  SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHig 60
Stone, D.M., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment of tumour
Partent: WO 0153466-A 11 26-JUL-2001;
Genentech, Inc. (US)
                                                                                                                  2482
205
0
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Matches:
Conservative:
Mismatches:

    .2482
    /organism="Homo sapiens"
/mol type="unassigned DNA"
    /db_xref="taxon:9606"

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Job time : 3737 secs
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1163.00
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Best Local Similarity:
Query Match:
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092F82 091E82 091A146 03973 09470 096703 09H1S3 084ZF1 084ZF1

069582

Q26358 Q9QY97 Q9VUE1 Q8NSZ6 Q9CQH0 Q923382 Q9UZ3 Q9VQT9 Q9VQT9 Q9VQT9

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0727d2 homo sapien
099344 mus musculu
099304 mus musculu
078748 oryza sativ
08h2v9 oryza sativ
08h2v9 oryza sativ
08h2v9 coryza sativ
09h2v9 homo sapien
09czv9 mus musculu
09czv9 mus musculu
09veg2 drosophila
09vvd1 bos taurus
08dfg vibrio vuln
08fg vibrio para
099t16 staphylococ
000420 homo sapien
08xxx5 ralstonia s
                                                                                                                                                    April 22, 2004, 10:14:05; Search time 65 Seconds (without alignments) 999.950 Million cell updates/sec
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1 MERRHPVCSGTCQPTQFRCS.....TVSTTEDTEHLVYNHTTRPL 206
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9D3K4
Q9D3K4
Q9D3K4
Q7KR46
Q8T2V9
Q9H813
Q9C2V9
Q9C7VD1
Q9VEGZ
Q9TVD1
Q9VEGZ
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Gapop 60.0 , Gapext 60.0
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sp_bacteria:*
sp_bungi:*
sp_human:*
sp_invertebrate:*
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sp_plant:*
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Match Length DB
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us-09-935-390a-23.01i.rspt

Q9D3K4

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SEQUENCE FROM N.A.

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STAIN=FVB/N-3; TISSUE=Breast tumor;

KITAIN=FVB/N-3; TISSUE=Breast tumor;

KITAIN=FVB/N-3; TISSUE=Breast tumor;

KITAIN=FVB/N-3; TISSUE-Breast L.H., Derge J.G.,

KITAIN=FVB/N-3; TISSUE-Breast L.H., Shenmen C.M., Schuler G.D.,

Alschuls R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Alschild R.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,

Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Appleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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R HSSP; P05067; 1CA0.

R GO; 001008233; Spint1.

R GO; GO:0004867; F:serine protease inhibitor activity; IEA.

GO; GO:0004867; F:serine protease inhibitor activity; IEA.

R InterPro; IPR002223; Kunitz_BPTI.

R InterPro; IPR00172; LDL ecceptor_A.

R Fam; PF00014; Kunitz_BPTI.

R PRINT; PR00057; Idl recept a: 1.

R PROMISS; RASTCPTASE.

R PROMISS; RASTCPTASE.

R PROMISS; PR00122; Kunitz_BPTI; 2.

R PROMISS; PR00229; BPTI KUNITZ_1; 2.

R PROSITE; PS00280; BPTI KUNITZ_2; 2.

R PROSITE; PS00280; BPTI KUNITZ_2; 2.

R PROSITE; PS00280; IDLRA_1; 1.

R PROSITE; PS0068; LDLRA_2; 1.

R PROGENCE SO7 AA; 56590 MW; P7F9CCF2693DIRBD CRC64;
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Q99J04 PRELIMINARY; PRT; 507 AA.
Q99J04;
Q1-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 25, Last annotation update)
Serine protease inhibitor, kunitz type 1 (Spint1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC005769; AAH05769.1; -. EMBL; BC05341; AAH5341.1; -. HSSP; P05067; ICA0.
                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local Similarity 100.0%; Pred. No. ...
Matches 40; Conservative 0; Mismatches
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STRAIN=FV3/N-3; FISSUB=Breast tumor;
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Strain Carraines Strong No. 1 (1992)

Strain Carraines Strong No. 1 (1992)

Revai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Atwai J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S., Alzawa X., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Atawa M., Sishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Atabi P., Lewis S., Marsuno Y., Nikaido I., Pesole G., Quackenbush J., Rochim P., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., A Sakai K., Okido T., Puruno M., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P., Ancrone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Shruki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Whyshaw-Boris A., Yoshida K., Haysshizaki Y., Nature 409:685-690(2001).

Nature 409:685-690(2001).

Nature 409:685-690(2001).

Nature 409:685-690(2001).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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MGD; MGI:1338033; Spintl.

GO:0004867; F:serine protease inhibitor activity; IEA.

InterPro; IPR002223; Kunitz BPTI.

InterPro; IPR002123; LDL receptor A.

Pfam; PF00014; Kunitz BPTI; 2.

Pfam; PF00057; Idl recept a; 1.

PRINTS; PR00759; BASICPTASE.

SMART; SM00131; KU; Z.

SMART; SM00191; LDLa; 1.
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PROSITE; PS50279; BPTI KUNITZ 2; 2.
PROSITE; PS01209; LDLRA 1; 1.
PROSITE; PS5068; LDLRA 2; 1.
Procease inhibitor; Serine protease inhibitor.
SEQUENCE 507 AA; 56571 MW; 9EE0A29B7056D72D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 CARPTYGGCYGNKNNFEEEQQCLESCRGISKKDVFGLRRE 132
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                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. v...
'... 0; Mismatches
                                                                                                                                                                                                                 507 A.A.
                                                                                                                                                                                                                                                                                                                                          Serine protease inhibitor, kunitz type 1. SPINT1.
                                 121 ISKKDVFGLRREIPIPSTGSVEMAV 145
                                                                                                                                                                                                                 PRT;
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Best Local Similarity
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AC CODD34
DD COL-JU

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RESULT 3 Q99J04

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us-09-935-390a-23.oli.rspt

RESULT 4

07XR48

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180gai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Takabama M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takabashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Yamamoto J., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Isayanagi T.;
"NibO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
Masuho Y., Kanehori K.;
Wabuho Y., Kanehori K.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Bypothetical protein.

SEQUENCE 350 AA, 39956 MW; D7BS975C34C9398C CRC64;
                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unional (Trimbline). 16, Created)
01-MAR-2001 (Trimbline). 16, Last sequence update)
01-MAR-2002 (Trimbline). 22, Last annotation update)
Hypothetical protein FL/14004.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
3.9%; Score 8; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels
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EMBL, BC006320; AAH06320.1; -.
Hypothetical protein.
SEQUENCE 350 AA; 40043 MW; 5F68ACA21DDD0674 CRC64;
                                        01-0CT-2000 (TYEMBLrel. 15, Created)
01-0CT-2000 (TYEMBLrel. 15, Last sequence update)
01-0CT-2002 (TYEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ10874.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.9%; Score 8; DB 4; Best Local Similarity 100.0%; Pred. No. 6.3; Matches 8; Conservative 0; Mismatches
350 A.A.
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PRELIMINARY;
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                                                                                                                                                                                                             NCBI_TaxID=9606;
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Q9NV85
Q9NV85;
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                                Q7XR48 PRELIMINARY; PRT; 390 AA.
Q7XR48;
Q7XR48;
Q1-CT-2003 (TrEMBLrel. 25, Created)
Q1-CT-2003 (TrEMBLrel. 25, Last sequence update)
Q1-CT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-CT-2003 (TrEMBLrel. 25, Last annotation update)
Q5JNBA0043A12.37,
G5JNBA0043A12.37.
G7XRA sativa (Rice).
Brkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enhantoidee; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Ehrhartoideae, Oryzeae, Oryza.
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Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC clone:oSJNBbD0011E04.";
Submitted (UNN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005443; BAC22566.1; -...
SEQUENCE 250 AA; 27639 MW; 60DA333BAD5822FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%; Score 9; DB 10; Length 390;
100.0%; Pred. No. 0.55;
tive 0; Mismatches 0; Indels
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Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 4.7
Matches 8; Conservative 0; Mismatches
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01-MAR-2003 (TrEMBLrel. 23, Ct
01-MAR-2003 (TrEMBLrel. 23, La
01-MAR-2003 (TrEMBLrel. 23, La
CSJNBb0011B04.11 protein.
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Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
A Ruehl P., Lewis S., Macsuo Y., Gissi C., King B., Kochiwa H.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Washer J., Washio T.,
Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J. Bult C., Fletcher C., Fulita M., Gariboldi M.,
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Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Saxamcto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.,
"Punctional annotation of a full-length mouse cDNA collection.";
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SEQUENCE FROM N.A.
SETALMS=CS7BL/60; TISSUE=Retina, Spinal cord, and Testis;
MEDLINE=2234663; PubMed=12466851;
The FANTOM CONSORTIUM.
The RIKEM Genome Exploration Research Group Phase I & II Team;
the RIKEM Genome Exploration Research Group Phase I annotation of 60,770 full-length oDNAs.;
MALUE 420:563-573(2002).
MALUE 420:563-573(2002).
EMBL; AK091270; BAC7730.1; ---
EMBL; AK091270; BAC7730.1; ---
EMBL; AK044482; BAC31946.1! ---
EMBL; AK044641; BAC7330.1; ---
EMBL; AK044641; BAC3383.1; ---
MGD; MGI:1914200; 2310026N02Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Bukaryota; Mustazoa; Arthropoda; Haxaoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      % Match 3.9%; Score 8; DB 11; Length 350; Local Similarity 100.0%; Pred. No. 6.3; les 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40178 MW; 3EE2CFBE929AE003 CRC64;
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01-0CT-2002 (TIEMBLrel. 22, Last sequence update)
01-JUN-2003 (TIEMBLrel. 24, Last annotation update)
CG16766 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 350 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Alzawa T., Izawa M., Nishi K., Kiyosawa H., Nondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori P., Bono H., Kasukawa T., Saito R., Kačota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Racota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Pistola H., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrill E., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrill E., Staubli F., Suzuki R., Tomita M., Wagner E., Washio T., Purumo M., Aono H., Baldarelli R., Barsh G., Bakai K., Okido T., Furumo M., Aono H., Baldarelli R., Barsh G., Bakai K., Shill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima M., Roditguez I., Sakamoto N., Lyons P., Marchionni L., Mashima M., Roditguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Wayashizaki Y., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Marchional annotation of a full-length mouse CDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851;
Mawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
2310028N02Rik protein (RIKEN CDNA 2310028N02 gene) (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
EMBL, AROL2107; BAEASO38.1, -.
MGD, MGI-1914200, 2310028N02Rik.
SEQUENCE 350 AA, 40285 MN; 12FD43319660775B CRC64;
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                             350 AA
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                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Embryo;
MBDEINE-21085660; PubMed-11217851;
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2310028N02RIK.
Mus musculus (Mouse).
Eukaryote; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17,
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                                                                                                                                                                                                                                                                                                                                  2310028N02Rik protein.
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                                                                                                                                                                                                                                                                                                                                                                                                               (Mouse)
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Matches 8; Conserv
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090771

RESULT 9

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Gaps

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Pfam; PF00001; 7tm 1; 1.

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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M., Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Barctor B. Botchan M.R., Bouck J., Brokstein P., Bolshakov S., Burtis R.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I., R.A. Burtis R.C., Dawles B., Delicher A., Danke C., Davemport L.B., Davies P., A de Pablos B., Delicher A., Dang Z., Mays A.D., Dew I., Dietz S.M., Boodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Barris N.J., Evangelista C.C., Ferraz C., Gabrielta A.E., Garg N.S., Galbart W.M., Glasser K., R. Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., Alaris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., Alali M., Kalush F., Karpen G.H., Kazi, K., Kanison J.A., Katchin K.A., Martei B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Raktei B., McInteoh T.C., Morris J., Moshrefi A., Markuei B., McInteoh T.C., Morris J., Moshrefi A., Markuei B., McInteoh T.C., Morris J., Moshrefi A., Mortwo G., Milshian N.V., Mobarry C., Morris J., Moshrefi A., Rahason D.K., Nakon K., Nakon K., Pacleb T.M., Rese M.G., Palazzolo M., Pittran G.S., Pan S., Pollard J., Puri V., Rese M.G., Sten B.C., Sten B.C., Sten B.C., Stapleton M., Strong R., San B., Spier E., Spradling A.C., Stapleton M., Strong R., San E., Spradling A.C., Stapleton M., Strong R., Wang A.H., Wang X., Milliams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q., And J., And J., March S., Pollard J., Wang S., Pollard J., March S., Pollard J., Wang S., Yao Q., Zheng L., Sheng R., Weinstock G.M., Wang A.H., Wang C., Wang K., March S., Pollard J.C., Stapleton W., Strong W., Zhou X., Zhon W., Wang S., Yao Q., Zheng L., Sheng S., Pollard J.C., Stapleton W., Strong W., Zhou X., Zhu S., Zhon W., Wang S., Wao Q., Zhong W., Shence 287:2185-2195(2000).
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FlyBase; FBgn0038541; CG16766.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
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A Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Barzon J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,
A Periters S., Frise B., Galle R.F., Gorge W.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A.,
A McIntosh T.C., Moy M., Park S., Patel S., Pfeiffer B., Rohnedson S., Scheeler P.,
A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler P.,
A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.W., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.",
L. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu i., Campbell K.,
Mistra S., Crosby M.A., Kaminker J.S., Prochnik S.B., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B.,
Clamp M., Drysdale R., Emmert D., Prise B., de Grey A., Harris N.,
Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith B., Millburn G., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Wungall C.J., Lewis S.B.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.

TISSUE-Adrenal medulla;

MEDLINE-9028564; PubMed=1693949;

Wu H.J., Parmer R.J., Koop A.H., Rozansky D.J., O'Connor D.T.;

Wu H.J., Parmer R.J., Koop A.H., Rozansky D.J., O'Connor D.T.;

Molecular cloning, structure, and expression of dopamine beta-
hydroxylase from bovine adrenal medulla.";

J. Neurochem. 55:97-105(1990).
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GO; GO:0005507; P:copper ion binding; IEA.
GO; GO:000584; P:catechOlamine metabolism; IEA.
InterPro; IPR000323; Cu2_monoxygenase.
InterPro; IPR000345; DB monoxygenase.
InterPro; IPR0008977; PHM PNGase F.
Pfam; PR01082; Cu2_monoxygen; I.
Pfam; PR01082; Cu2_monoxygen; I.
Pfam; PR0312; Cu2_monoxygen; I.
Pfam; PR0312; Cu2_monoxygen; I.
Pfam; PR0312; Cu2_monoxygen; I.
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                                                                                             Length 586;
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                                                                                                                             Indels
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TISSUE=Adrenal medulla;
Wu H.J., Parmer R.J., Koop A.H., Rozansky D.J., O'Connor
Submitrad (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI18633, AAD09829.1; -.
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CF89D62A9472B7C6 CRC64;
            PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECRE F1 1; 1.
PROSITE; PS5024; GPROTEIN RECREPF1 2; 1.
SEQUENCE S86 AA; 64897 NM; BEB9C75EEGB3844F CRC64;
                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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100.0%; Pred. No. 9.9;
iive 0; Mismatches
                                                                                          Query Match 3.9%; Score 8; DB 5; Best Local Similarity 100.0%; Pred. No. 9.8; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                             597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS00084, CU2 MONOOXYGENASE 1; 1. PROSITE, PS00085, CU2 MONOOXYGENASE 2; 1.
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                                                                                                                                                                                                                                                                                                                                                           Dopamine beta-hydroxylase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      597 AA; 66685 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00767; DBMONOXGNASE.
SMART; SM00664; DOH; 1.
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Matches 8; Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        597
                                                                                                                                                              144 AVAVFLVI 151
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                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                              09TVD1;
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                                                                                                                                                                                                                                                                             09TVD1
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RESULT 12

Length 758;

DB 16;

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Complete proteome.
SEQUENCE 758 AA; 82555 MW; BEEGE07BCEB8663D CRC64;
                                                                                            Query Match
3.9%; Score 8; DB 16
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches
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Q99TL6;
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SEQUENCE FROM N.A.

SEQUENCE FROM S.A.

MEDLINE=22508454; PubMed=12620739;

MACHINE=22508454; PubMed=12620739;

MACHINE=22508454; PubMed=12620739;

MACHINE=22508454; PubMed=12620739;

MACHINE Y., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Machino K., Oshima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
of stinct from that of V. cholerae.";

Lancet 361:743-749(2003).

RABL, AR005075; BAC59121.1;

RABL, AR005075; BAC59121.1;

RO; Go:0015093; Fiferrous iron transport; IEA.

GO; Go:0015093; Fiferrous iron transport; IEA.

MITCEPPC; IPR003773; FeoB.

InterPrc; IPR00373; FeoB.

RITCEPPC; IRR060673; GTP1_OBG.

REALL; PR00326; GTP10BG.
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A. Rhee J.H., Xim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
T. Complete genome sequence of Vibrio vulnificus CMCP6 ";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
R. EMBL, ARO18686.1;
R. CO, GO:0015093; F.ferrous iron transporter activity; IEA.
GO; GO:0015694; F.ferrous iron transport; IEA.
N. GO: GO:0015694; F.ferrous iron transport; IEA.
N. GO:0015694; F.ferrous iron transport; IEA.
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Sasteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae; Vibrionaceae; Vibrio.
WCBI_TaxID=670;
                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=672;
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                                                            QBDFQ8;
01-MRR-2003 (TrEMBLrel. 23, Created)
01-MRR-2003 (TrEMBLrel. 23, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Fe2+ transport system protein B.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Ferrous iron transport protein B.
                                   758 A.A.
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TIGRFAMS; TIGR00231; small_GTP; 1.
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SEQUENCE 758 AA
                                   QBDFQ8
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STRAIN
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Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 4, Last sequence update)
Protein-export membrane protein SetDF.
SECF OR SAVIGET ON SALIGE ON RAMISST.
Staphylococcus aureus (strain Muso / ATCC 700699),
Staphylococcus aureus (strain Muso / ATCC 700699),
Staphylococcus aureus (strain Muso / Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620,
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PRINTS; PR01755; SECTRANCASE.
TIGREAMS; TIGR00916; 2A0604801; 2.
TIGRFAMS; TIGR01129; SecD; 1.
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                                                                                                      153 IVVVVAIL 160
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SEQUENCE 759 AA;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
BEDGERGIN J.B., McCready P.M., Adamson A.A., Burkhart-Schultz K.,
Lamerdin J.B., McCready P.M., Atilwagen S., Garnes J., Danganan L.,
Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
Carrano A.V.;
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01.JUL-1997 (TrEMBLrel. 04, Last sequence update)
01.JUN-2003 (TrEMBLrel. 24, Last annotation update)
E19541 (Fragment).
ENDS F19541 (Fra
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Best Local Similarity 100.
Matches 8; Conservative
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688 IVVVVAIL 695
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Search completed: April 22, 2004, 10:25:16 Job time : 68 secs

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R. J. Biol. Chem. 272:63/U-63/6:1291).
R. J. Biol. Chem. 272:63/U-63/6:1291).
R. SEQUENCE FROM N.A.
R. TSSTSE-COLOn, and Placenta;
R. STSTSE-COLOn, and Placenta;
R. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
R. Alsurent R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
R.A. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
R.A. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
R.A. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
R.A. Expleton M.J., Usdin T.B., Foshiyuki S., Carninci P., Prange C.,
R.A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.U.,
R.A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.U.,
R.A. Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
R.A. Rahayan R.W., Touchman J.W., Gremer B.D., Dickson M.C.,
R.A. Schnerch A., Schmutz J., Myers R.M.,
R.A. Schnerch A., Schmutz J., Myers R.M.,
R.A. Schnerch A., Schmutz J., Myers R.M.,
R.A. Schnerch A., Schmutz J., Warra M.A.,
R.A. Schnerch A., Schmutz J., Warra W.A.,
R.A. Human and mouse cDNA sequences.",
R. Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
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chlorella v
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anthopleura
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             pseudorabie
                             nomo sapien
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Lin C.Y., Anders J., Johnson M., Dickson R.B.;
Lin C.Y., Anders J., Johnson M., Dickson R.B.;
Purification and characterization of a complex containing matriptase and a Kunitz-type serine protease inhibitor from human milk.";
J. Biol. Chem. 274:18277-1842(1999).
-!- FUNCTION: Inhibitor of HGF activator. Also acts as an inhibitor of matripease (ST14).
                                                                                                                                                                                                                                                            SPT1_HUMAN STANDARD; PRT; 513 AA.
043278;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
115-WAR-2004 (Rel. 43, Last annotation update)
Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor spinyt) RAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J
Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.;
Hepatocyte growth factor activator inhibitor, a novel Kunitz-type
serine protease inhibitor.";
J. Biol. Chem. 272:6370-6376(1997).
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
           P33485
000555
P22052
P26227
P81547
P00976
Q9muv4
Q9E10w0
P5610w0
Q9E1060
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MEDLINE=97197808; PubMed=9045658;
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SPT1_HUMAN
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                                                                                       April 22, 2004, 09:32:14 ; Search time 18 Seconds [without alignments] 595.914 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                             US-09-935-390A-23
206
1 MERRHPVCSGTCQPTQFRCS......TVSTTEDTEHLVYNHTTRPL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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P55316 F
P55315 P
000939 1
0000987 1
091080 P
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060500 N
029670 d
Q13113 N
P77551 d
Q48630 J
043570 N
P56260 d
P71345 N
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P38568
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O14934
O54853
P35875
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035219
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPT1 HUMAN
SPT1 MOUSE
LRP2 BATT
DOPO BOYTN
NPHN HUMAN
YSSS ARCFU
MA17 HUMAN
AZPR BCOLI
CAHČ HUMAN
QIN ĀVES
BRNÖ_HABIN
ÇINĀ ĀVES
BRNÖ_HABIN
PXGB_HUMAN
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PXGB_HUMAN
PXGB_HUMAN
PXGB_MOUSE
PXGB_MOUSE
K6B1_HUMAN
K6B1_RAT
HYAP_MACPA
NCPR_MUSDO
SL52_HUMAN
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CANFA
HUMAN
                                                               - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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SPT1 MOUSE
09R097;
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CARBOHYD
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SEQUENCE
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEXYTSGFDELQRIH 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNNFEEEQQCLESCRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 FPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNNFEEBQQCLESCRG 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 ISKKDVFGLRREIPIPSTGSVEMAVAVFLVICIVVVVAILGYCFFKNQRKDFHGHHHHPP 487
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N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

M, DGEOSF3A58BSCDDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  KUNITZ-TYPE PROTEASE INHIBITOR 1.
PRIJKUNITZ INHIBITOR 1.
LDL-RECEPTOR CLASS A.
BPTI/KUNITZ INHIBITOR 2.
                                                                                                                                                                                                                       R GO; GO:0005576; C:extracellular; TAS.

R GO; GO:0005524; C:membrane fraction; TAS.
GO; GO:0005624; C:membrane fraction; TAS.
GO:0006667; F:serine procease inhibitor activity; TAS.
R InterPro; IPR002172; LDL receptor A.
R Pfam; PR00014; Kunitz BPTI.
R PFR00175; LDL receptor A.
R PRINTS; PR00759; BASICPTASE;
R PRINTS; PR00759; BASICPTASE;
R SWART; SW00131; Kui; 2.
R PROSITE; PR00280; BPTI KUNITZ 1; 2.
R PROSITE; PS00280; BPTI KUNITZ 1; 2.
R PROSITE; PS00280; LDLRA 1; 1.
R PROSITE; PS00280; LDLRA 2; 1.
R PROSITE; PS00280; LDLRA 2; 1.
R SEXINE PROSITE; PS01209; LDLRA 2; 1.
R SEXINE PROSITE; PS01209; LDLRA 2; 1.
R SEXINE PROSITE; PS01209; LDLRA 2; 1.
R SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 206; DB 1; Length 513; 100.0%; Pred. No. 4.5e-215; ive 0; Mismatches 0; Indels 0
          DOWAIN: This inhibitor contains two inhibitory domains. SIMILARITY: Contains 1 LDL-receptor class A domain. SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIPASSIVSTIEDIEHLVYNHITRPL 206
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 SUBCELLULAR LOCATION: Secreted
                                                                                                                                                    EMBL, AB000095; BAA25014.1; -. EMBL; BC004140; AAH04140.1; -. EMBL; BC018702.3; AAH18702.1; -. HSSP; P31713; LSHP.
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235
507
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384
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566
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513 AA;
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DISULPID
DISULPID
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DISULFID
ACT SITE
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DISULFID
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Best Local
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                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor activator inhibitor type 1) (HAI-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Itch H., Kataoka H., Meng J.Y., Hamasuna R., Kitamura N., Koono M.
"Mouse hepatocyte growth factor activator inhibitor type 1 (HAI-1)
and type 2 (HAI-2) placental bikumin genes and their promoters.";
Blochim. Blophys. Acta 1519:99-95(2001)
- FUNCTION: Inhibitor of HGF activator (By similarity).
- SUBCELULIAR LOCATION: Secreted (By similarity).
- SUBCELULIAR Inhibitor contains two inhibitory domains.
- SIMILARITY: Contains 1 LDL-receptor class A domain.
- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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BYI/KUNITZ INHIBITOR 2.
BY SIMILARITY.
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BPTI/KUNITZ INHIBITOR 1.
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MOD; MOISTON, Spintl.
InterPro; IPR00213; Kunitz BPTI.
InterPro; IPR002172; LDL receptor_A.
Pfam; PF00014; Kunitz BPTI; 2.
Pfam; PF00015; Idl recept_a; 1.
PRINTS; PR0075; ldl recept_a; 1.
PRNOTS; PR00122; Kunitz_BPTI; 2.
SWART; SW0011; KU; 2.
SWART; SW0019; LDLa, 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS00280; LDLA, 1.
PROSITE; PS0008; LDLRA_2; 1.
PROSITE; PS0008; LDLRA_2; 1.
SGAINE DECORAGE INDLRA_2; 1.
SGAINE DECORAGE INDLRA_3; 1.
SGAINE DECORAGE INDRA_3; 1.
SGAINE DECORAGE IND
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507 AA
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MEDLINE=21299055; PubMed=11406276;
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STANDARD;
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Best Local Similarity
Matches 40; Conserv
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444646666
   HSSP; Q07954; 1CR8.
GlycoSuiteDB; P98158;
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DOMAIN
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WEDLINE-9472242; PubMed=7510321;

MEDLINE-9472242; PubMed=7510321;

MEDLINE-9472242; PubMed=7510321;

Andres G., McCluskey R.T.;

Andres G., McCluskey R.T.;

Andres G., McCluskey R.T.;

Togan distribution in rate of two members of the low-density

Togan distribution in rate of two members of the low-density

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Togan distribution in rate of two members of the low-density

Togan distribution in rate of two members of the low-density

Togan distribution in rate of two members of the low-density and candid and calcium.

Togan distribution in mannogly-ossides and polymyrin B.

Togan distribution in main of the call membrane protein. Expressed in clawarde at the call surface.

Togan distribution in main of polymyrin in membrane protein. Expressed in clawarde at the call surface.

Togan distribution in main in soluble form is possibly derived by proximal tubule, lung, epididymis, yolk sac, among others.

Togan distribution in minine in BGF-like domains.

SIMILARITY: Contains 37 LDL-receptor class B domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                  01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Low-density lipoprotein receptor-related protein 2 precursor (Megalin)
(Glycoprotein 330) (9p330).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95386696, PubMed=7544804,
Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E.,
Norris K., Gliemann J., Christensen E.I.;
"Evidence that epithelial glycoprotein 330/megalin mediates uptake of
polybasic drugs.",
J. Clin. Invest. 96:1404-1413(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley; TISSUE-Kidney; MEDLINE=95024033; PubMed=7937880; Saito A., Pietromonato S., Loo A.K.C., Farquhar M.G.; "Complete cloning and sequencing of rat gp330/'megalin,' a distinctive member of the low density lipoprotein receptor
CARFIYGGCYGNKNNFBEEQQCLESCRGISKKDVFGLRRE 132
                                 CARFIYGGCYGNKNNFEEEQQCLESCRGISKKDVFGLRRE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).
                                                                                                                                                                                                 PRT; 4660 AA
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P98158;
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EMBL; L34049; AAA51369.1; -.

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EGF-LIKE 5.

EGF-LIKE 6, CALCIUM-BINDING (FOTENTIAL).

LDL-RECEPTOR CLASS B 10.

LDL-RECEPTOR CLASS B 12.

LDL-RECEPTOR CLASS B 13.

LDL-RECEPTOR CLASS B 13.

LDL-RECEPTOR CLASS B 14.

EGF-LIKE 7.

LDL-RECEPTOR CLASS B 15.

LDL-RECEPTOR CLASS B 15.

LDL-RECEPTOR CLASS B 15.

LDL-RECEPTOR CLASS B 16.

LDL-RECEPTOR CLASS B 17.

LDL-RECEPTOR CLASS B 17.

LDL-RECEPTOR CLASS B 17.

LDL-RECEPTOR CLASS B 17.
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                                                                                                                                                                                                                                                                      PROSITE; PSO0010; ASX_HYDROXYL; 4.
PROSITE; PSO0010; ASX_HYDROXYL; 4.
PROSITE; PSO10186; EGF_1; 1.
PROSITE; PSO1187; EGF_2; 8.
PROSITE; PSO1187; EGF_2; 3.
PROSITE; PSO1109; LDLRA, 3.
PROSITE; PSO068; LDLRA_2; 36.
Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane; Ecoptor; EGF-11ke domain; SH3-binding; Signal.
SS POTENTIAL.
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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IDI.-RECEPTOR CLASS B 2
IDI.-RECEPTOR CLASS B 2
IDI.-RECEPTOR CLASS B 3
IDI.-RECEPTOR CLASS B 5
IDI.-RECEPTOR CLASS B 5
IDI.-RECEPTOR CLASS B 6
IDI.-RECEPTOR CLASS B 7
IDI.-RECEPTOR CLASS B 9
IDI.-RECEPTOR CLASS B 9
IDI.-RECEPTOR CLASS B 9
IDI.-RECEPTOR CLASS B 9
IDI.-RECEPTOR CLASS A 9
IDI.-RECEPTOR CLASS A 1
IDI.-R
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LDL-RECEPTOR CLASS A 2
LDL-RECEPTOR CLASS A 3
LDL-RECEPTOR CLASS A 4
LDL-RECEPTOR CLASS A 5
LDL-RECEPTOR CLASS A 5
LDL-RECEPTOR CLASS A 7
LDL-RECEPTOR CLASS A 7
EQF-LIKE 1.
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EGF-LIKE 8.
LDL-RECEPTOR C
                                         InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR001891; EGP_Ca.
InterPro; IPR00209; EGP_like.
InterPro; IPR0020172; LDL receptor_rep.
InterPro; IPR00133; Ldl_receptor_rep.
Pfam; PR00108; EGP; 9.
Pfam; PR00108; Idl_recept_b; 33.
PR0015; Idl_recept_b; 33.
SMART; SM01192; LDLa; 36.
SMART; SM01192; LDLa; 36.
SMART; SM001192; LDLa; 36.
PROSITE; PS00010; ASX HYDROXYL; 4.
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                   NEDLINE-90110081; PubMed=1688549;
Lewis E.J., Allison S., Rader D., Claflin V., Baizer L.;
"Bovine dopamine beta-hydroxylase cDNA. Complete coding sequence and expression in mammalian cells with vaccinia virus vector.";
J. Biol. Chem. 265:1021-1028(1990).
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                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation update)
Dopamine beta-monooxygenase precursor (RC 1.14.17.1) (Dopamine beta-
                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE OF 33-610.
MEDLINE=90110082; PubMed=2295597;
Robertson J.G., Desai P.R., Kumar A., Farrington G.K.,
Fitzpatrick P.F., Villafranca J.J.;
Fitzpatrick P.F., Villafranca J.J.;
Fitzpatriary amino acid sequence of bovine dopamine beta-hydroxylase.";
J. Biol. Chem. 265:1029-1035 (1990).
                                                                                                  Boss taurus (Bovine).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Advend medula;
MEDLINE-77134133; MEDLINE-77134133;
Skotland T., Ljones T., Flatmark T., Sletten K.;
"NH-terminal Bequence of dopamine beta-hydroxylase from bovine adrenal medulla.";
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              610 AA
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Taylor C.S., Kent U.M., Fleming P.J.;
"The membrane-binding segment of dopamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monooxygenase family.
-!- SIMILARITY: Contains 1 DOMON domain.
                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90148928; Pubmed=2620060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uncleaved signal sequence.";
J. Biol. Chem. 264:14-16(1989)
              STANDARD;
                                                                                   hydroxylase) (DBH)
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CLASS B 35.
CLASS B 37.
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LDE-RECEPOR CLASS A 31.
LDE-RECEPOR CLASS A 31.
LDE-RECEPOR CLASS A 33.
LDE-RECEPOR CLASS A 34.
LDE-RECEPOR CLASS A 35.
LDE-RECEPOR CLASS A 36.
RGF-LIKE 14.
RGF-LIKE 15.
CALCIUM-BINDING (POTENTIAL).
LDE-RECEPOR CLASS B 35.
LDE-RECEPOR CLASS B 36.
LDE-RECEPOR CLASS B 37.
CLASS B 37.
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
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Pred. No. 0.006;
LDL-RECEPTOR C
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100.0%; Pre
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Best Local Similarity
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RESULT

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SEQUENCE FROM N.A. (ISOFORM 1)
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Nephrin precursor (Renal glomerulus-specific cell adhesion receptor).
NPHS: OR NPHN.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
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Q -> H (IN REF. 2).
1639DB670F94DE71 CRC64;
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N-LINKED (GLCNAC. ..).
P -> T [N REF. 4].
P -> T (N REF. 4].
SWN -> RYV (IN REF. 3).
L -> F [N REF. 3].
C -> R (IN REF. 2).
RDH -> ETI (IN REF. 2).
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POTENTIAL.
COPPER (POTENTIAL)
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PRINTS, PR00767, DBWONOXGNASE.
AMRYF, SMO0664, DDH, 1.
PROSITE, PS00084; CTZ MONOXYGENASE 1; 1.
PROSITE; PS00085; CTZ MONOXYGENASE 2; 1.
PROSITE; PS50836; DOMON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.9%; Score 8;
                                                                                                                                                            InterPro; IPR000323; Cu2 monooxygnse.
InterPro; IPR000945; DB monoxygenase.
InterPro; IPR005018; DOMON.
InterPro; IPR005018; DOMON.
Pfam; PP03312; Cu2 monoox C; I.
Pfam; PP01082; Cu2 monooxygen; I.
                                                                                                                EMBL; J02890; AAA30356.1; -.
EMBL; J05160; AAA30490.1; ALT_INIT.
HSSP; P14925; 1PHM.
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les 8; Conser
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NPHN HUMAN
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MEDLINEs-20117947; PubMed-2015;
Aya K., Tanaka H., Seino Y.;
Kidney Int. S7:401-404(2000).

-!- FUNCTION: Seems to play a role in the development or function of the kidney glomerular filtration barrier. May anchor the podocyte slit diaphragm to the actin cytoskeleton.
-!- SUBUNIT: Interacts with podocin/NPHS2. Interacts with CD2AP C-terminal domain (By similarity).
-!- SUBCELILIAR LOCATION: Type I membrane protein (Potential).
Predominantly located at podocyte slit diaphragm between podocyte foot processes. Also associated with podocyte apical plasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99324171; PubMed=10393930;
Ructsalainen V., Ljungberg P., Wartiovaara J., Lenkkeri U.,
Kestilae M., Jalanko H., Holmberg C., Tryggvason K.;
"Nephrin is specifically located at the slit diaphragm of glomerular
MEDLINE=99325371; PubMed=9660941;
Restilae M., Lenkkeri U., Maennikkoe M., Lamerdin J., McCready P.,
Putaala H., Ructalainen V., Morita T., Nissinen M., Herva R.,
Rashtan C.B., Peltonen L., Holmberg C., Oleen A., Tryggvason K.;
"Postitionally cloned gene for a novel glomerular protein -- nephrin is mutated in congenital nephrotic syndrome.";
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THR-172 DEL, ARG-366; CYS-367; SRR-368; VAL-376; GLN-408; TYR-465;
PRO-350; ARG-366; CYS-310; PRB-523; CYS-724; CYS-743; TRP-802; PRO-802;
ASP-806; CYS-811 AND CYS-1140.
MEDLINE=99115081; PubMed=9915943;
MEDLINE=99115081; PubMed=9915943;
MIDLINE=99116081; PubMed=9915943;
MIDLINE=99116081; Antignac C.K., Kashtan C.E., Homberg C., Olsen A., Kestilae M., Tryggvason K.;
Xestilae M., Tryggvason K.;
Structure of the gene for congenital nephrotic syndrome of the Finnish type (NPHS1) and characterization of mutations.";
Am. J. Hum. Genet. 64:51-61(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holthoefer H., Ahola H., Solin M.-L., Wang S.-X., Palmen T., Luimmla P., Miettinen A., Kerjaschki D., Weptinen B., Kerjaschki D., Weptinen localizes at the podocyte filtration slit area and is characteristically spliced in the human kidney."; Am. J. Pathol. 155:1681-1687(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21551283; PubMed=11562357;
Huber T.B., Kottgen M., Schilling B., Walz G., Benzing T.;
"Interaction with podocin facilitates nephrin signaling.";
                                                                                                                                                                                                                                                                                                                           [2] SEQUENCE FROM N.A. (ISOPORM 1).
STUURNER FROM N.A. Kumar N., Kalluri R.;
Grunkemeyer J.A., Kumar N., Kalluri R.;
Fluman nephrin (NPHS1) cDNA sequence.";
Fluman nephrin (NPHS1) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 96:7962-7967(1999).
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Event=Alternative splicing; Named isoforms=2;
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[6]
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MEDLINE=20019662; PubMed=10550324;
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COULD BE A POLYMORPHISM)
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343;
NIBOLINE=98049343;
NIBOLINE=98049343;
NIBOLINE=98049343;
NIBOLINE=98049343;
NIBOLINE N.A., Dodson R.A., Gwinn M., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1241;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
  Missing (in isoform 2)
/FIId=VSP 002598.
W -> S (IN CNF).
/FIId=VAR_013029.
                                                                                                                            /FTIG=VAR 013033.
/FTIG=VAR 013033.
TPR -> I [IN CNF].
/FTIG=VAR 013034.
G -> C (IN CNF).
                                                                                                                                                                                                                                                                                               /FIId=VAR 013039.

L -> V (IN CMP).

FTId=VAR 013040.

R -> Q (IN CMP; COI

/FIId=VAR 013041.

FTId=VAR 013042.

/FIId=VAR 013042.

C -> Y (IN CMP).
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/FTId=VAR 013038.
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FTId=VAR 013035.
S -> P (IN CNF).
FTId=VAR 013036.
S -> R (IN CNF).
FTIG=VAR 013037.
R -> C (IN CNF).
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MISSING (IN CNF).
/FTId=VAR 013032.
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ID Y585_ARCFU
AC 029670
DT 16-0CT-2001 (Rel. 40, Last sequence update)
DT 16-0CT-2001 (Rel. 40, Last annotation update)
DF 16-0CT-2001 (Rel. 40, Last annotation update)
DF 16-0CT-2001 (Rel. 40, Last annotation update)
DF H905hetical protein AP0585.
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FTId=VAR 013030
:-> N (IN CNF).
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C -> F (IN CNF).
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S -> C (IN CNF).
/FTId=VAR 013047
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/FTId=VAR_01
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      EMBL; AF035835; AAC3968711; -.

BR EMBL; AF035837; AAC3968711; -.

BR EMBL; AF190637; AAC3141.1; -.

BR EMBL; AF190637; AAC3141.1; -.

BR EMBL; AF190637; AAC3141.1; -.

BR EMBL; AF190637; AAC31651.1; -.

BR EMBL; AF1906716; -.

BR Genew; HGNC:7008; NPHSI.

MIM, 502716; -.

BR GO; GO:0007155; P:excretion; TAS.

GO; GO:00071589; P:excretion; TAS.

GO; GO:00071598; P:excretion; TAS.

GO; GO:00071598; P:excretion; TAS.

GO; GO:00071598; P:excretion; TAS.

BR InterPro; IPR003967; FN III-11ke.

BR InterPro; IPR003167; Ig-11ke.

BR InterPro; IPR003598; Ig-22.

BR Ffam; PP00041; fn3; 1.

BR Ffam; PP00041; fn3; 1.

BR SMART; SM00408; IG-22.

BR SMART; SM00408; IG-22.

Cell adhesion; Transmembrane; Signal; Glycoprotein;

GW Disease mutation; Polymorphism.

THENDRAIN

TH
podocytes of the periphery of mature and developing glomeruli. PTM: Phosphorylated on tyrosine residues.
BISEASE: Defects in NPHS: are the cause of congenital nephrotic syndrome of the Finnish type (NPHS) or CNF) [MIM:256300]; an autosomal recessive disorder characterized by massive proteinuria in utero and nephrosis at birth.
SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 1 fibromectin type III domain.
SIMILARITY: Contains 8 immunoglobulin-like domains.
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 1.

PRENONECTIN TYPE-III.

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Gaps

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STRAIN=K12 / MG1655;
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TRANSMEM
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RZPR OR B1362.
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AC P77551;
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                                                                                                                                                                                                                                            This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    Loftus B.,
ak A., Zhou L.,
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=2388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heigh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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MEDLINE=99034932; PubMed=9815914;
MEDLINE=99034932; PubMed=9815914;
Kocher O., Cheresh P., Brown L.F., Lee S.W.;
"Identification of a novel gene, selectively up-regulated in human carchnomas, using the differential display technique.";
Clin. Cancer Res. 1:1209-1215(1995).
Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T. Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370 (1997).
-:- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; AF0585; -. Hypothetical protein; Transmembrane; Complete proteome.
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KARLOLLY
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LD MA17 HUMAN

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CO 013113; 096E11,
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 17 kDa membrane associated protein (DD96 protein).
CS Mammalia; Eutheria; Primates; Craniata; Vertebrata; E Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
CN NCBL TaxID=9606;
RN MEDLINE=99034922; PubMed=9815914;
RA KOCHER CO., Cheresh P., Brown L.F., Lee S.W.;
RY MEDLINE=99034932; PubMed=9815914;
RY MEDLINE=99034932; PubMed=9815914;
RY Carcinomas, using the differential display technique.
RL Clin. Cancer Res. 1:1209-1215(1995).
RL SUDMITCALION N.A.
R. Graffham D.,
R. Graffham D.,
R. Graffham D.,
R. Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databas
RN [3]
RN SEQUENCE FROM N.A.
RA Graffham D.,
RA Altanber R.D., Collins F.S., Magner L., Shemmen C.M.,
RA Altanber R.D., Collins F.S., Magner L., Shemmen C.M.,
RA Altanber R.D., Collins F.S., Magner L., Wangn G.N.,
RA HODKINS-22388257; PubMed=12477932;
RA Altanber R.D., Collins F.S., Magner L., Shemmen C.M.,
RA HOBKINS R.P., Jordan H., Moore T., Mang J.,
RA HOBKINS R.P., Jordan H., Moore T., Mang J.,
RA HOBKINS R.P., Jordan H., Moore T., Mang J.,
RA Hobkins R.P., Jordan H., Moore T., Mang J.,
RA Hobkins R.P., Jordan H., Moore T., Rabin G.M.,
RA Hobkins R.P., Jordan H., Moore T., Rabin G.M.,
RA Hobkins R.P., Jordan H., Moore T., Rabin G.M.,
RA Hobkins R.P., Jordan H., Moore T., Rabin G.M.,
RA Hobkins R.P., Jordan H., Rabin G.M.,
RA Hobkins R.P., Jordan H., Rabin G.M.,
RA Hobkins R.P., Jordan H., Moore T., Wangner T.L.,
RA Hobkins R.P., Jordan H., Rabin G.M.,
RA Rabin R. R. J., Jordan H., Rabin G.M.,
RA Rabin R. R. J., Jordan H., Rabin G.M.,
RA Rabin R. R. J., Jordan R., Rabin G.M.,
RA Rab
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100.0%; Pred. No. 3.5;
tive 0; Mismatches
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67 89
90 AA; 10081 MW;
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Matches 7; Conservative
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                                                                                                                                         Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                       Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McZwan P.J., McZwarnan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzry D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmitz J., Myers R.M., Schmitz J., Myers R.M., Schmitz J., Myers R.M., Schmitz J., Mores B.M., Schmitz J., Jones S.J.M., Marra M.A.; Feneration and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."
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LoCT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Putative Rz endopeptidase from lambdoid prophage Rac (EC 3.4...-)
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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N -> K (IN REF. 3).
7DEB64C3AF78CB18 CRC64;
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100.0%; Pred. No. ...
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13
51 N
12227 MW;
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Best Local Similarity 100...
Best Local 7; Conservative
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13
51
114 AA;
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membrane protein (Potential).
  LOCATION: Integral membrane
Belongs to the dedA family.
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                                                                                                                                                                                                                      EMBL, Z29065; CAAB2306.1; -. PIR, S39339; S39339; EMBL S39339; Deda. InterPro; IPR000252; Deda. Pfam; PP00597; Deda, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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tes 7; Conserv
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SUBCELLULAR
SIMILARITY:
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SEQUENCE
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CAHC HUMAN
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                                                                                                                                                                         STRAIN=K12;

MEDLINE=9725137; PubMed=9097039;

MEDLINE=9725137; PubMed=9097039;

MEDLINE=9725137; PubMed=9097039;

MEDLINE=9725137; PubMed=9097039;

MEDLINE=9725137; PubMed=9097039;

MEDLINE=9725137; PubMed=8.0. Kitakawa M., Kitagawa M.,

Kasai H., Kashimoto K., Kimura S., Mitakawa M., Moriu T., Mocomura K.,

Makino K., Miki T., Misobuchi K., Mori H., Mori T., Mocomura K.,

Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,

Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,

Rampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,

Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;

"A 570-kb DNA sequence of the Bscherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";

I. DNA Res. 3:363-377(1996).

I. FUNCTION: Necessary for host cell lysis. It is believed to code
for an endopeptidase that cleaves the amino-carboxyl cross-link
between the diaminopimelic acid and D-alamine residues in the
murch component of the bacterial cell wall (By similarity).

C.-I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY UB. STRONG, TO LAWBDOID
PHAGES ENDOPEPTIDASES.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
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MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III; Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE000233, AAC74444.1, ALT_INIT.

EMBL, D90774, BAA14959.1, ALT_INIT.

Ecodene, EQ13366, rzpR.

Interpro. IPR04929, Phage lysis.

Pfam, PF03245, Phage lysis, 1.

Hypothetical protein, Hydrolase, Protease, Bacteriolytic enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                "The complete genome sequence of Bscherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 3.4%; Score 7; DB 1; Length 147; Local Similarity 100.0%; Pred. No. 5.5; Onservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 147 AA; 16486 MW; 2F4E85F6663A7692 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-ROV-1997 (Rel. 35, Last sequence update)
Alkaline phosphatase like protein.
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NCBI_TaxID=1359;
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Q48630;
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SEQUENCE !
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Matches
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1D APL LACLC

1D APL LACLC

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TISSUE—EVe, and Kidney;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
TISSTE=PREMAL Cell carcinoma;
MEDLINE=98301622; PubMed=9636197;
TUBETCECI O., Sahin U., Vollmar E., Siener S., Goettert E., Seit Parkkila A.-K., Sahah G.N., Grubb J.H., Pfreundschuh M., Sly W. "Human carbonic anhydrase XII: CDNA cloning, expression, and chromosomal localization of a carbonic anhydrase gene that is overxpressed in some renal cell cancers.";
Proc. Natl. Acad. Sci. U.S.A. 95:7608-7613(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 242;
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141 161 POTENTIAL.
177 197 POTENTIAL.
242 AA; 27134 MW; 650A8B314C44BA55 CRC64;
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100.0%; Pred. No. 8.7;
tive 0; Mismatches
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(POTENTIAL). (POTENTIAL). (POTENTIAL).

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Length 354;
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262 263
269 287
285 287
354 AA; 39451 MW; 9016216BP2CA6COC CRC64;
                                          N-LINKED (GLCNAC. .) ()
N-LINKED (GLCNAC. .) ()
N-LINKED (GLCNAC. .) ()
Missing (in isoform 2).
/FTIG-VSP_000772.
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QIN AVIS3
ID QIN AVIS3
STANDARD; PRT; 387 AA.
AC P56560;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DF Transforming protein Qin (Oncogene Qin).
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100.0%; Pred. No. 12;
ive 0; Mismatches
   ZINC (CATALYTIC)
ZINC (CATALYTIC)
ZINC (CATALYTIC)
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Best Local Similarity 100.
Matches 7; Conservative
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SEQUENCE
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CARBOHYD
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellaro N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Modan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Cong A., C., Shevchenko Y., Bouffard G.G., A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Human and mouse cDNA sequences.",
I. Human and mouse cDNA sequences.",
I. Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903 [2002].
                                                                                                                                                     Name 2. Isold = 043570-2; Sequence = VSP 000772; Nowe 2. Isold = 043570-2; Sequence = VSP 000772; Note = No experimental confirmation available; INCERTY = VEROITY: HIGHLY EXPRESSED IN COLON, KIDNEY, PROSTATE, INTESTINE AND ACTIVATED LYMPHOCYTES. EXPRESSED AT MOCH HIGHER LEVELS IN THE RENAL CELL CANCERS THAN IN SURROUNDING NORMAL KIDNEY FISSUE. MODERATELY EXPRESSED IN PANCREAS, OVARY, AND TESTIS. SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBONIC ANHYDRASE XII.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 603263; -.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0004089; F:carbonate dehydratase activity; TAS.
GO; GO:000408270; F:zinc ion binding; TAS.
InterPro; IPR001148; Buk COanhd.
Pfam; PF00194; carb_anhydrase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                               Name=1;
IsoId=043570-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000865; Euk Cóanhd; 1.
PROSITE; PS00162; EUK CO2 ANHYDRASE; 1.
Lyase; Zinc; Transmembrane; Signal; Alt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF051882, AAC39789.1; -.
EMBL, AF037335, AAC6955.1; -.
EMBL, BC000278.1; -.
EMBL, BC011691; AAH11691.1; -.
EMBL, BC021981, AAH11691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1JD0; 17-AUG-01.
PDB; 1JCZ; 17-AUG-01.
Genew: HGNC:1371; CA12.
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354
322
354
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SIGNAL
CHAIN
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Gaps

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                                                                                                                                 "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                          Science 269:496-512(1995).

-!- FUNCTION: Component of the transport system for branched-chain amino acids (leucine, isoleucine and valine) Which is coupled to proton motive force (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: BELONGS TO THE BRAC/BRAZ/BRNQ FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Puhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2104 (Rel. 43, Last annotation update)
Transcription factor BF-1) (Brain factor 1) (BF1) (CBF-1)
ONCOGENE C-QIN (N-62-5) (CBQ 3-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PPOS525; Branch AA trans; 1.
TIGRRAMs; TIGR00796; Iivos; 1.
Amino-acid transport; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%; Score 7; DB 1; Length 436; 100.0%; Pred. No. 15;
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MEDLINE=95132616; PubMed=7831308;
Chang H.W., Li J., Kretz8chmar D., Vogt P.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA.
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POTENTIAL.
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Eukaryota, Metazoa, Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 VVVAILG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 ,
436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 VVVAILG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
TRANSMEM 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR, HI0226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FXGB CHICK
090964;
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                                                                                                               Venter J.
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TRANSMEM
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                                                                                                                                                          Rd. ";
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15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoutation update)
Branched-chain amino acid transport system carrier protein (Branched-chain amino acid uptake carrier).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
                             Avian sarcoma virus (strain 31) (ASV31).
Viruses, Retroid viruses, Retroviridae, Avian type C retroviruses.
NCBL_TaxID=35270;
                                                                                                                                                   Li J., Vogt P.K.;
"The retroviral oncogene qin belongs to the transcription factor family that includes the homeoric gene fork head.";
Proc. Natl. Acad. Sci. U.S.A. 90:4490-4494 (1993).
-: SUBCELLULAR LOCATION: Nuclear.
-: MISCELLANBOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-QIN
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-ALA.
POLY-ALA.
FORK-HEAD.
FRA902F50FFE42F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      日 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Q61245; znr...

TRANSFAC; T01832; ...
InterPro; IPR001766; ...
PRINTS; PR00150; Pork head; 1.

R PRODOM; PD000425; FP Fork head; 1.

R PRODOM; PD000425; FP Fork head; 1.

R PROSITE; PS00657; FORK HEAD 1; 1.

R PROSITE; PS00657; FORK HEAD 2; 1.

R PROSITE; PS0069; FORK HEAD 2; 1.

R PROSITE; PS00139; FORK HEAD 2; 1.

R PROSITE; PS00139; FORK HEAD 2; 1.

RW PAD-binding; Nuclear protein; Oncogene.

FW PROSITE; PS00139; FORK HEAD 2; 1.

RW PROSITE; PS00139; FORK HEAD 2; 1.

RW PROSITE; PS00139; FORK HEAD 2; 1.

RW PROSITE; PS00139; FORK HEAD 2; 1.

FROMALN 1.
                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 fork-head domain.
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100.0%; Pred. No. 13;
ive 0; Mismatches
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HSSP; Q63245; 2HFH.
                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93281605; PubMed=8099441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 AA; 42283 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHHHPPP 181
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Best Local Similarity
Matches 7; Consery
                                                                                                                                                                                                                                                                                          POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=727;
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SEQUENCE
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RESULT 12 BRNQ HAEIN

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Gaps

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                                                                                                                                                                                                                   MEDLINE-9522450; PubMed=7599184; MEDLINE-9522450; PubMed=7599184; MEDLINE-9522450; PubMed=7599184; Misse S., Murphy D.B., Schlung A., Burfeind P., Schmundt D., Schnulle V., Mattei M.-G., Thies U.; and 2, members of the fork head schmulle V. Mattei M.-G., Thies U.; and 2, members of the fork head gene family, are clustered on chromosome 14q."; Biochim. Biophys. Acta 1262:105-112(1995).

-!-FUNCTION: Plays an important role in the establishment of the regional subdivision of the developing brain and in the development of the telencephalon. Sequence-specific DMA-binding protein with a distinct binding specificity (By similarity).
-!-SUMCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                     Murphy D.B., Wiese S., Burfeind P., Schmundt D., Mattei M.-G.,
Schulz-Schaeffer W., Thies U.;
"Human brain factor 1, a new member of the fork head gene family.";
                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                               Length 469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIS-RICH.
PRO-RICH.
POLY-GIN.
POLY-ARG.
PORK-HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO0657; FORK HEAD_1; 1.
PROSITE; PSO0658; FORK HEAD_2; 1.
PROSITE; PSO0658; FORK HEAD_2; 1.
Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4%; Score 7; DB 1;
100.0%; Pred. No. 16;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 600779; -... Goldon, TAS. GO; GO:0003677; F:DNA binding; TAS. GO; GO:0007420; P:Drain development; TAS. InterPro; IPR001766; TF Fork head. Pfam; PF00250; Fork head; 1. PRODONS; FORKHEAD. PRINTS; PR000353; FORKHEAD. SMART; SM00339; FH; I.
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79 PR(
73 PO]
88 PO]
252 FO]
50539 MW;
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EMBL; X74143; CAA52240.1; -.
PIR; I37451; I37451.
HSSP; Q63245; 2HFH.
TRANSPAC; T02292; -.
Genew; HGNC:3811; FOXG1A.
                                                                                                                                                                                     Genomics 21:551-557(1994).
[2]
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Best Local Similarity
7; Conserve
       sapiens (Human)
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469 AA;
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                                                                                     SEQUENCE FROM N.A.
                                                     NCBI_TaxID=9606;
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FXGE HUMAN
ID FXGE HUMAN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the Buropean Bioinformatics Institute. There are or estrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                               consequently specify the topographical projection of the retinal consequently specify the topographical projection of the retinal canding angulon-cell axons to the tectum by controlling expression of their target genes.

-! SIMELLULAR LOCATION: Nuclear (Potential).
-! TISSUE SPECIFICITY: Retina and brain.
-! DEVELOPMENTAL STAGE: Can be detected in regions including prinordial retina and neuroepithelium by embryonic day 2 (R2). At E3, expressed in the nasal retina and pigment epithelium as well as in the telencephalon, and at E7 is expressed in retinal ganglion cells. Levels begin to decline from E4 and almost disappear by E10.
-! SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                 SEQUENCE FROM N.A.
STRAIN=White leghorn; TISSURE-Retina;
MEDLINE-6338226; PubMed-8757134;
Yuasa J., Hirano S., Yamagata M., Noda M.;
"Vistal projection map specified by topographic expression of
transcription factors in the retina.";
Nature 382:632-635(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; ASS909; ASS909.
HSSP; Q63245; 2HFH.
TRANSFAC; T01833; .
TRANSFAC; T01833; .
TRANSFAC; PRO0250; FORK head; 1.
PEAM; PF00250; FORK head; 1.
PROMOM; PD000045; TF FORK head; 1.
PROSITE; PS00053; FORK HEAD 1.
PROSITE; PS00056; FORK HEAD 1; 1.
PROSITE; PS00059; FORK HEAD 1; 1.
TRANSCITE; PS00059; FORK HEAD 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Forthead box protein GlA (Forkhead-related protein FKHL2)
(Transcription factor BF-2) (Brain factor 2) (HFK2).
FOXGIA OR FKHL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4%; Score 7; DB 1; Length 451;
100.0%; Pred. No. 15;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E9E5B407D2321B50 CRC64;
"Avian cellular homolog of the qin oncogene."; Proc. Natl. Acad. Sci. U.S.A. 92:447-451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 AA
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FORK-HEAD.
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POLY-ALA.
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EMBL; U47275; AAB08466.1; -.
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nes 7; Conservative
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58
67
106
233
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64
103
142
251 AA;
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SEQUENCE
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FXGA HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;

MEDLINE=9532450; PubMed=7599184;

MEDLINE=9532450; PubMed=7599184;

Mises S., Murphy D.B., Schlung A., Burfeind P., Schmundt D.,

Schmulle V., Mattei M.-G., Thies U.;

The genes for human brain factor 1 and 2, members of the fork head

The genes for human brain factor 1 and 2, members of the fork head

The genes for human brain factor 1 and 2, members of the fork head

The genes for human brain factor 1 and 2, members of the fork head

The genes family, are clustered on chromosome 14g.";

Biochim. Biophys. Acta 1262-115-112(1995).

The genes family, are clustered on chromosome 14g.";

The genes family are clustered on chromosome 14g.";

The genes family, are clustered on chromosome 14g.";

The genes family are clustered on chromosome 14g.";

The genes family, are clustered on chromosome 14g.";

The genes family are clustered on chromosome 14g.";

The genes family are clustered on chromosome 14g.";

The genes family are clustered on chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MBD&INE=95048332; PubMed=7959731;
Murphy D.B., Wiese S., Burfeind P., Schmundt D., Mattei M.-G.,
Schulz-Schaeffer W., Thies U.;
Fuman brain factor 1, a new member of the fork head gene family.";
Genomics 21:551-557(1994).
                                                                                                                                                                                                                                                                         Homo Sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM, 164874; ..., Good State of the control of the 
                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Forkhead box protein G1B (Forkhead-related protein FKHL1)
(Transcription factor BF-1) (Brain factor 1) (BF1) (HFK1)
FOXG1B OR FKHL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.4%; Score 7; DB 1; Length 477; Best Local Similarity 100.0%; Pred. No. 16; Matches 7; Conservative 0; Mismatches 0; Indels
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PRO-RICH.
POLY-GIN.
POLY-LEU.
FORK-HEAD.
W, 71CFD0BD069CFADS CRC64;
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TRANSFAC; T02350; -.
Genew; HGNC:3812; FOXGIB.
MIM; 164874; -.
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477 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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54 HHHHPPP 60

Search completed: April 22, 2004, 10:24:02 Job time : 19 secs

175 KEHHPPP 181

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 22, 2004, 10:15:30 ; Search time 26 Seconds (without alignments) 762.133 Million cell updates/sec Run on:

US-09-935-390A-23
206
1 MERRHPVCSGTCQPTQFRCS.....TVSTTEDTEHLVYNHTTRPL 206 Title: Perfect score:

Scoring table: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0

283366 segs, 96191526 residues Searched:

0 Word size :

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | de | | | Saranas | |
|---------------|----------|----------------|--------|----|---------|--------------------|
| Result No. | Score | Query Match | Length | ÐB | ID | Description |
| | 11 | 5.3 | 972 | ~ | A30363 | glycoprotein GP330 |
| 7 | 11 | 5.3 | 4660 | ~ | T42737 | gp330 protein prec |
| m | œ | w o. | 610 | ~ | A33650 | dopamine beta-mono |
| 4 | σο | 9.0 | 759 | ~ | D89946 | |
| ហ | œ | 9.0 | 1241 | 7 | T37190 | nephrin - human |
| 9 | œ | 9.0 | 1743 | 7 | T26859 | hypothetical prote |
| ۲- | 7 | 3.4 | 90 | N | A69323 | |
| æ | r | 3.4 | 116 | ~ | E48338 | hypothetical prote |
| σv | 7 | 3.4 | 135 | 7 | G97172 | |
| 10 | 7 | 3.4 | 152 | N | 849230 | glycine cleavage s |
| 11 | 7 | 3.4 | 159 | ~ | T38729 | hypothetical prote |
| 12 | 7 | 3.4 | 161 | ~ | 860198 | leave |
| 13 | 7 | 3.4 | 173 | N | A72620 | probable NADH dehy |
| 14 | 7 | 3.4 | 202 | 7 | D87019 | cytochrome C oxida |
| 15 | 7 | 3.4 | 217 | N | AI3429 | transposase BME114 |
| 16 | 7 | 3.4 | 221 | ~ | S20964 | ribosomal protein |
| | 7 | 3.4 | 222 | 7 | T03540 | cobalamin biosynth |
| 18 | 7 | 3.4 | 222 | 7 | H96711 | hypothetical prote |
| | 7 | 3.4 | 242 | ~ | 839339 | alkaline phosphata |
| | 7 | 3.4 | 256 | 7 | H36857 | B26R protein - var |
| 21 | 7 | 3.4 | 281 | N | T20743 | ical |
| | L | 3.4 | 283 | ~ | B69713 | |
| 23 | 7 | 3.4 | | N | T17737 | ne-rich |
| 24 | 7 | 3.4 | 317 | N | AC0464 | c |
| | 7 | 3.4 | | N | E89836 | cal g |
| | 7 | 3.4 | 368 | N | T36414 | probable iron-side |
| 27 | 7 | 3.4 | 387 | N | A47446 | HNF-3/fork head fa |
| . 58 | 7 | 3.4 | 388 | N | T18937 | |
| 59 | 2 | 3.4 | 394 | N | T20633 | hypothetical prote |

| hypothetical prote hypothetical prote | branched-chain ami transforming prote | serine-type carbox HBF-G2 (HFK-2) pro | transcription fact brain factor 1 pro | p70 S6 kinase (EC conserved hypothet | | probable ribosomal | sulfate permease (hypothetical prote |
|------------------------------------------|------------------------------------------|------------------------------------------|---------------------------------------|--------------------------------------|------------------|--------------------|--------------------------------------|
| T21188 B81417 | D64056 A55909 | S51516 I37451 | A54743 JH0672 | JE0377 E96024 | A41687 TVRTK6 | S12906 | AB2766 P97546 |
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ALIGNMENTS

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RESULT 2 T42737 셤

91330 protein precursor - rat
NyAlternate names: megalin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42737
R;Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994

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A;Wolecule type: protein
A;Residues: 33-37 <TAY>
R;Skotland, T.; Ljones, T.; Flatmark, T.; Sletten, K.
Biochem. Biophys. Res. Commun. 74, 1483-1489, 1977
A;Title: NH-2-terminal sequence of dopamine beca-hydroxylase from bovine adrenal medull
A;Reference number: Al2853; MUID:77134133; PMID:843373
                                                                                                                                                                A;Status: preliminary
A;Nolecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 33-55, RrV', 59-63;73, F', 75-411;420-441;445-465;468-559, 'C', 561-563;566-605
B;Residues: 33.855, RRV', J.M.; Fleming, P.J.
J. Biol. Chem. 264, 14-16, 1989
A;Title: The membrane-binding segment of dopamine beta-hydroxylase is not an uncleaved
A;Ritle: The membrane-binding segment of dopamine beta-hydroxylase is not an uncleaved
A;Reference number: A31802; MUID:89079641; PMID:2909511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-export membrane protein SecDF (imported) - Staphylococcus aureus (strain N315) C; Species: Staphylococcus aureus (strain N315) C; Species: Otaphylococcus aureus (strain N315) C; Accession: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogn ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A; File: Mole genome sequencing of meticillin-resistant Stapylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Actacus: Description of meticillin-resistant Stapylococcus aureus. A;Actacus: Description of MUD:21311952; PMID:11418146
A;Actacus: preliminary
A;Molecule type: DNA
A;Reddidus: 1-759 <KUR>
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        J. Biol. Chem. 265, 1029-1035, 1990
A/Title: Primary amino acid sequence of bovine dopamine beta-hydroxylase.
A/Reference number: A34926; MUID:90110082; PMID:2295597
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C,Genetics:
A,Gene: secF
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Best Local Similarity 100.
Matches 8; Conservative
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A, Fitle: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of d, Reference number: A58173; MUID:95024033; PMID:7937880
A, Accession: T4273; MUID:95024033; PMID:7937880
A, Accession: T4273;
A, Residual: T4279; translated from GB/EMBL/DDBJ
A, Residual: Lype: mRNA
A, Residual: Lype: MRNA
A, Residual: Lype: MRNA
A, Cross-references: ERBL:134049; NID:9561852; PID:9561853; PIDN:AAA51369.1
A, Experimental source: strain Sprague-Dawley; Kidney
C, Superfamily: alpha-2-marcoglobulin receptor; BGF homology; LDL receptor ligand-binding
F, 1-25/Domain: signal sequence #status predicted <SIG>F, 26-4660/Product: gp330 protein #status predicted <NAT>
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A; Residues: 33-34, T', 36-44, X', 46-47, TX', 50 <SKO>
A; Residues: 33-34, T', 36-44, X', 46-47, TX', 50 <SKO>
A; Residues: 33-34, T', 36-44, X', 46-47, TX', 50 <SKO>
A; Residues: 33-34, T', 36-44, X', 46-47, TX', 50 <SKO>
A; Repertantal source: adrenal medulla
A; Note: residue 46 was also sequenced as lee
A; Robertson, J.G.; Adams, G.W.; Medzihradszky, K.F.; Burlingame, A.L.; Villafranca, J.C.
B; Robertson, J.G.; Adams, G.W.; Medzihradszky, K.F.; Burlingame, A.L.; Villafranca, J.C.
A; Title: Complete assignment of disulfide bonds in bovine dopamine beta-monocxygenase catalyzes the biosynthetic conversion of dopamin C; Comment: Dopamine beta-monocxygenase at tetrameric glycoprotein bound in both the n C; Comment: Dopamine beta-monocxygenase is a tetrameric glycoprotein; monot in both the n C; Comment: Dopamine beta-monocxygenase is a tetrameric glycoprotein; monot in both the n C; Superfamily: peptidylglycine monocxygenase is membrane-bound form #status predicted <WI
C; Superfamily: peptidylglycine monocxygenase; membrane-bound form #status predicted <WI
F; 1-32, Domain: signal sequence #link Mrff #status predicted <AGA
F; 200-fordain: signal sequence #link Mrff #status predicted
F; 227, Active aite: Tyr #status predicted
F; 227, Active aite: Tyr #status predicted
F; 223, Disulfide bonds: interchain #status predicted
F; 221, 522, Disulfide bonds: interchain #status predicted
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100.0%; Pred. No. 4.4;
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C;Accession: A6923
E;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L. Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-90 <a href="https://doi.org/10.1004/">https://doi.org/10.1004/</a> A;Residues: 1-90 <a href="https://doi.org/10.1004/">https://doi.org/10.1004/</a> A;Cross-references: GB:AE001064; GB:AE000782; NID:g2689387; PIDN:AAB90659.1; PID:g26501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein orf71 - equine herpesvirus 4 (strain 405/76) (fragment)
C;Species: equine herpesvirus 4
C;Species: equine herpesvirus 4
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 08-Oct-1999
C;Accession: E48338
R;Nagesha, H.S.; Crabb, B.S.; Studdert, M.J.
Arch. Virol. 128, 143-154, 1993
A;Title: Analysis of the nucleotide sequence of five genes at the left end of the unique A;Reference number: A48338 MUID:93119267; PMID:8380320
A;Accession: E48338
A;Status: preliminary
A;Mosidues: 1-16 cMAP
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(997172

hypothetical protein CAC2213 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Bate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Date: 1097172

R;Nolling, U; Beton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
B;Nolling, W.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
Batteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325
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A, Residues: 1-135 < XUR>
A, Cross-references: GB; AB001437; PIDN: AAK80170.1; PID:g15025210; GSPDB:GN00168
A, Experimental source: Clostridium acetobutylicum ATCC824
C, Genetics:
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A,Note: seguence extracted from NCBI backbone (NCBIN:121741, NCBIP:121746)
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3.4%; Score 7; DB 2; Length 116;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 0; Indels
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3.4%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches
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Anticellar Cell 1, 575-582, 1998

Molecular Cell 1, 575-582, MUID:98325371, PMID:9660941

A;Recession: T37190

A;Recession: T37190

A;Residues: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-1241 <KES>
A;Residues: 1-1241 <KES>
C;Genetics:
A;Residues: BMBL:AF035835; NID:g3025698; PIDN:AAC39687.1; PID:g3025699
C;Genetics:
A;Gene: NPHS1

A;Map position: 19
A;Mote: mutated in congenital nephrotic syndrome of the Finnish type (NPHS1); located in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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Kestila, M.; Lenkkeri, U.; Mannikko, M.; Lamerdin, J.; McCready, P.; Putaala, H.; Ruod
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26859
R;Anscough, R.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20278
A;Reference number: Z20278
A;Accession: T26859
A;Status: preliminary; translated from GB/BMBL/DDBJ
A;Residues: 1-1743 *WIL>
A;Residues: 1-1743 *WIL>
A;Coss-references: EMBL:AL032623; PIDN:CAA21511.1; CBSP:Y43FBB.3
A;Coss-references: Clone Y43FBB
C;Genetics:
A;Genetics:
A;Genetics:
A;Chitrons: 65/1; 92/2; 128/1; 229/1; 367/2; 34/2011; 486/2; 523/1; 571/1; 628/1; 857/2;
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                          .Species: Homo sapiens (man)
.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
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Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches
                                     Query Match 3.9%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.9%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 7.9; Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                      153 IVVVVAIL 160
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proble NADH dehydrogenase (ubiquinone) chain 6 APE1418 - Aeropyrum pernix (strain K1.) proble NADH dehydrogenase (ubiquinone) chain 6 APE1418 - Aeropyrum pernix (; Species: Aeropyrum pernix (; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence 6 #s. Fundahan, Y.; Hano, Y.; Hano, Y.; Hanakan, Y.; Hano, Y.; Takanya, M.; Masuda, Y.; Hano, Y.; Fundahan, Y.; Takanya, Y.; Takanya, M.; Masuda, S.; Fundahanhi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; N.; Reference number: A72450; MUD:99310339; PMID:10382966 #sequence number: A72450; 
                                                                                                                                                                                                                                                      glycine cleavage system protein H precursor (clone HFP13) - Flaveria pringlei (fragment N;Alternate names: H-protein C;Species: Flaveria pringlei C;Species: Flaveria pringlei C;Species: Flaveria pringlei C;Accession: S60198 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999 R;Ropriva, S.; Bauwe, H.
                                                                                                                                                                                                                                                                                                                                                                                                                        Kropriva, S.; Bauwe, H.

Kropriva, S.; Bauwe, H.

Mol. Gen. Genet. 249, 111-116, 1995

My Title: M-protein of glycine decarboxylase is encoded by multigene families in Flaver: My Efference number: S60194; MUID: 96140454; PMID: 8552027

My Reference number: S60198

A, Reference number: S60198

A, Molecule type: DNA

My Molecule type: DNA

My Residues: 1-161 < KODP>

My Experimental source: EMBL: Z37522; NID: 9547499; PIDN: CAA85759.1; PID: 9547500

My Residues: Source: tissue type leaf

My Rote: the nucleotide sequence was submitted to the EMBL Data Library, September 1994

C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology C;Keywords: lipoamide C;Keywords: lipoamide (mitochondrion) (fragment) #status predicted <SIG>F;1-30/Domain: transit peptide (mitochondrion) (fragment) #status predicted <SIG>F;1-161/Product: glycine cleavage system protein H #status predicted <WAT>F;54-128/Domain: lipoyl/biotin-binding homology <LPB>F;93/Binding site: lipoamide (Lys) (covalent) #status predicted
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D87019
cytochrome C oxidase subunit III [imported] - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.4%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 17; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 VAVFLVI 151
SSTVSTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 VOLPDIG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 VDLPDTG 77
                                                                            SSTVSTT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Genome: nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Genetics:
A, Gene: APB1418
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185
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                                                               g
                                                                                                                                                                                                                                                                                                         Glycine cleavage system protein H precursor (clone HFC2) - Plaveria cronquistii
NyAlternate names: H-protein
NyAlternate names: H-protein
C;Species: Flaveria cronquistii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1897 #text_change 20-Aug-1899
C;Accession: S49230; S60197
C;Accession: S49230; S60197
C;Accession: Datue, H.
Submitted to the EMBL Data Library, September 1894
A;Pescription: Molecular cloning and comparative analysis of H-protein of glycine decark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: DNA
A Residues: 1-152 < KOD>
A; Residues: 1-152 < KOD>
A; Cross-references: ENEL: Z37518; NID: 9547518; PIDN: CAA85755.1; PID: 9547519
A; Cross-references: ENEL: 249; III-116, 1995
A; Title: H-protein of glycine decarboxylase is encoded by multigene families in Flaveria
A; Reference number: S60194; MJID: 96140454; PMID: 8552027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: T38729
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Accession: T38729
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DBA
A,Rolecule type: DBA
A,Rolecule type: DBA
A,Residues: 1-159 cdBA>
A,Cross-references: EMBL: Z99167; PIDN: CAB16286.1; GSPDB:GN00066; SPDB:SPAC3G6.10c
A,Experimental source: strain 972h-; cosmid c3G6
C,Genetics: SPDB:SPAC3G6.10c
A,Gene: SPDB:SPAC3G6.10c
A,Gene: SPDB:SPAC3G6.10c
A,Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC3G6.10c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Superfamily: glycine cleavage system protein H; lipoyl/biotin-binding homology C; Superfamily: glycine cleavage system protein H; status predicted <SIG> E;1-31/Domain: transit peptide (mitochondrion) #status predicted <SIG> E;32-152/Product: glycine cleavage system protein H #status predicted <WAT> F;55-129/Domain: lipoyl/biotin-binding homology  E;59-129/Domain: lipoyl/biotin-binding homology  Covalent #$94/Binding site: lipoamide (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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100.0%; Pred. No. 16;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Kesidues: 8-168 a kWh.
A,Cross-references: EMBL:237518
A;Experimental source: tissue type leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S60197
A;Status: translation not shown
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Best Local Similarity love.
Person 7; Conservative
                                              KKDVFGL 129
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                                                                                         KKDVFGL 38
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C;Species: Mycchacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: D87019
R;Cole, S.T.; Biglmeter, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A;Title: Massive gene decay in the leprosy bacillus.
A;Attence number: A66909; MUID:21128732; PMID:11234002
A;Accession: D87019
A;Accession: D87019
A;Accession: D87019
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3.4%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches
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RESULT 15
A13429
transposase BMEI1423 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Decies: Brucella melitensis
C;Decies: Brucella melitensis
C;Decies: Brucella melitensis
C;Decies: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A13429
R;DelYecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
N;DelYecchio, V.G.; Kapatral, V.; Redkar, R.J.; P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acd. Sci. U.S.A. 99, 443-448, 2002
A;Reference number: AD352; PMID:1175688
A;Reference number: AD352; PMID:1175688
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <kUR>
A;Molecule type: DNA
A;Residues: 1-217 <kUR>
A;Accession: A13429
A;Experimental source: strain 16M
A;Experimental source: strain 16M
A;Gene: BWEI1423
A;Map position: I

94 DVFGLRR 100

125 DVFGLRR 131

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Gaps

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0; Indels

Length 217;

DB 2;

Ouery Match
3.4%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches

142 EMAVAVF 148

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38 EMAVAVE 44

Search completed: April 22, 2004, 10:25:49
Job time : 28 secs

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April 22, 2004, 10:23:45; Search time 361 Seconds (without alignments) 157.767 Million cell updates/sec
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206
1 MERRHPVCSGTCQPTQPRCS.....TVSTTEDTEHLVYNHTTRPL 206
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                          OM protein - protein search, using sw model
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Perfect score:
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Published Applications AA:*

| Ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| Ggn2_6/ptodata/1/pubpaa/US06_MWF PUB.pep:*
| Ggn2_6/ptodata/1/pubpaa/US06_MWF PUB.pep:*
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| Ggn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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| Ggn2_6/ptodata/1/pubpaa/US0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | Sequence 23, Appl | Sequence 18, Appl | Sequence 2, Appli | Sequence 42, Appl | Sequence 10, Appl | Sequence 10, Appl | 12, | 42, | 10, | 10, | 10, | Sequence 10, Appl | Segmence 10, Appl | 10, | Sequence 10, Appl |
|-----------|--------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|-------------------|
| SUMMARIES | ID | US-09-935-390A-23 | US-09-765-449-18 | US-09-742-201-2 | US-10-081-056-42 | US-10-245-752-10 | US-10-245-859-10 | US-10-211-858-12 | US-10-305-654-42 | US-10-245-103-10 | US-10-245-107-10 | US-10-245-143-10 | US-10-245-771-10 | US-10-245-851-10 | US-10-245-883-10 | US-10-237-535-10 |
| | B O | σ | 0 | σ | 12 | 13 | 12 | 12 | 12 | 14 | 14 | 14 | 14 | 4 | 14 | 14 |
| | Query Match Length DB | 206 | 513 | 529 | 529 | 529 | 529 | 529 | 529 | 529 | 529 | 529 | 529 | 529 | 529 | 529 |
| de | Query Match | 100.0 | 100.0 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 |
| | Score | 206 | 206 | 145 | 145 | 145 | 145 | 145 | 145 | 145 | 145 | 145 | 145 | 145 | 145 | 145 |
| | Result No. | н | 2 | m | 4 | ιΩ | 9 | 7 | œ | σ | 10 | 11 | 12 | . 13 | 14 | 15 |

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| 238-183 238-283 245-140 245-140 245-140 245-130 245-130 245-130 245-130 245-130 245-431 245-431 245-431 245-431 245-431 245-431 245-431 245-431 245-431 245-431 245-431 245-431 245-431 245-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 246-431 |
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ALIGNMENTS

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Sequence 2, Application US/09742201

Sequence 2, Application US/09742201

Patent No. US20020123091A1

GENERAL INFORMATION:

APPLICANT: Gurney, Austin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: For Use in Modulation of Hepatocyte Growth Factor Act:

TITLE OF INVENTION: For Use in Modulation of Anglogenesis and Cardiovascularization

FILE REFERENCE: P1861R1US

CURRENT APPLICATION NUMBER: US/09/742,201

CURRENT FILING DATE: 2000-12-19

PRIOR PLING DATE: 2000-02-11

PRIOR PLING DATE: 2000-03-15

PRIOR PLING DATE: 2000-03-15

PRIOR PLING DATE: 2000-03-15

PRIOR PLING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 6

SEQ ID NOS: 6
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                                                                                                                                                            368 PPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNNFEBEQQCLESCRG 427
                                                                                                                                                                                                                                                                                                                 ISKKDVFGLRREIPIPSTGSVEMAVAVFLVICIVVVVAILGYCFFKNQRKDFHGHHHHPP 180
                                                                                                                                                                                                                                                                                                                                 428 ISKKOVPGLRREIPIPSTGSVEMAVAVFLVICIVVVVAILGYCFFKNQRKDFHGHHHHPP 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 MERRHPYCSGTCQPTQPRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARPTYGGCYGNKNNFBBBQQCLESCRG 120
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                                                                                                                                    1 MERRHPVCSGTCQPTQPRCSNGCCIDSFLECDDTPNCPDASDBAACEKYTSGFDELQRIH
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                                                 Length 513;
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                                                                                         Indels
                                          Score 206; DB 9; I
Pred. No. 1.9e-195;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                      PTPASSTVSTTEDTEHLVYNHTTRPL 206
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Sequence 42, Application US/10081056
Publication No. US20040043927A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
                                                                                         ö
                                               100.0%;
                                            Query Match
Best Local Similarity 100.
Matches 206; Conservative
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    US-09-765-449-18
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US-09-742-201-2
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ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMBUTER: 1BM FC compatible
COMBUTER: 1BM FC compatible
COMBUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION NUMBER: 08/685,558
FILING DATE: -CURNOWN-
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
LENGTH: 513 amino acids
                                                                                                                                                                                                                                                 Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHIMOMURA, Takeshi
KAMAGUCHI, Toshiya
KITAMURA, Naomi
MIYAZAWA, Keiji
MIYAZAWA, Keiji
TITLE OF INVENTION: ANOVEL PROTEIN, DNA CODING FOR SAME
                                                                                                                                                                                                                                              Query Match 100.0%; Score 206; DB 9; Length 2
Best Local Similarity 100.0%; Pred. No. 8.5e-196;
Matches 206; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
| TELEX: <Unknown>
| TELEX: <Unknown>
| INPORMATION FOR SEQ ID NO: 23:
| SEQUENCE CHARACTERISTICS:
| ENGTH: 206 amino acids
| TYPE: amino acidd
| STRANDENNESS: single
| TOPOLOGY: linear |
| MOLECULE TYPE: No. US200207561Ale
| SEQUENCE DESCRIPTION: SEQ ID NO: 23:
| US-09-935-390A-23
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SEQUENCE DESCRIPTION: SEQ ID NO: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIPASSTVSTTEDTEHLVYNHTTRPL 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09765449 Patent No. US20020098537A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: DC
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US-09-765-449-18
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ORGANISM: Homosapiens
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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APPLICANT: Watchabe. COLIN K.
APPLICANTON NUMBER: US/O1017-07-081.056
PRIOR APPLICATION NUMBER: US 60/121.556
PRIOR APPLICATION NUMBER: US 60/121.556
PRIOR APPLICATION NUMBER: US 60/121.566
PRIOR APPLICATION NUMBER: US 60/121.664
PRIOR APPLICATION NUMBER: US 60/121.697
PRIOR APPLICATION NUMBER: US 60/121.697
PRIOR APPLICATION NUMBER: PCT/US00/13673
PRIOR PLILICATION NUMBER: US 60/14/1299
PRIOR
                                                                                                                                                                         Pan, Jamee
Paoni, Nicholas F.
Stephan, Jean-Philippe F.
Waranabe, Colin K.
Wood, William I.
Gerber, Hanspeter
Gerlitsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Grimaldi,J. Christopher
APPLICANT: Grimaldi,J. Christopher
APPLICANT: Suchan, Jean-
APPLICANT: Suchan, Jean-
APPLICANT: Stephan, Jean-
APPLICANT: Stephan, Jean-
APPLICANT: Stephan, Jean-
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
APPLICANT: Lang, Zemin
APPLICANT: Lang, Zemin
APPLICANT: Pong, Sherman
APPLICANT: Pong, Sherman
APPLICANT: Pong, Sherman
APPLICANT: ACIDS ENCODING THB SAMB
FILE REFERENCE: D5630R1C6
CURRENT APPLICATION NUMBER: 10/197942
FRIOR APPLICATION NUMBER: 10/197942
FRIOR APPLICATION NUMBER: 60/063046
PRIOR APPLICATION NUMBER: 60/063046
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PRIOR APPLICATION NUMBER: US 09/828,386
PRIOR PLINING DATE: 2001-04-05
PRIOR PLINING DATE: 2001-05-10
PRIOR PLINING DATE: 2001-05-10
PRIOR PLINING DATE: 2001-05-10
PRIOR PLINING DATE: 2001-05-10
PRIOR PLINING DATE: 2001-05-25
PRIOR PLINING DATE: 2001-05-30
PRIOR PLINING DATE: 2001-06-30
PRIOR PLINING DATE: 2001-06-20
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Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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Publication No. US20030064473A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
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121 ISKKDVFGLRREIPIPSTGSVEMAV 145
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; Sequence 12, Application US/10211858
; Publication No. US20030211096Al
; GENERAL INFORMATION:
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APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pari, James
APPLICANT: Pitti, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo Sapien
US-10-245-859-10
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Best Local Simi
Matches 145;
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Publication No. US20030064474A1
GENERAL INFORMATION:
APPLICANT: Batch. Kevin
APPLICANT: Batch. Cevin
APPLICANT: Batch. Cevin
APPLICANT: Goldard, Audrey
APPLICANT: Gurey, Austin
APPLICANT: Gurey, Austin
APPLICANT: Gurey, Austin
APPLICANT: Alenghan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: And, William
APPLICANT: And, William
APPLICANT: And, Alliam
APPLICANT: And, Alliam
APPLICANT: And, Alliam
APPLICANT: And, Jean-Phillippe
APPLICANT: Pong, Sherman
APPLICANT: Pong, Sherman
APPLICANT: Pong, Sherman
APPLICANT: NOWERR: 10/10/245,859
CURRENT APPLICATION NUMBER: 10/10/245,859
CURRENT FILING DATE: 2002-07-18
FRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/09689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/09689
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PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR PELING DATE: 1997-11-10
PRIOR PELING DATE: 1998-03-11-10
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-14
PRIOR PILING DATE: 1998-06-14
PRIOR PILING DATE: 1998-06-14
PRIOR PILING DATE: 1998-06-14
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-14
PRIOR PILING DATE: 1998-06-15
PRIOR PILING DATE: 1998-06-16
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70.4%; Score 145; DB 12; Length 5
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Homo Sapien
US-10-245-752-10
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APPLICANT: ROY, MARGARE M.
APPLICANT: ROY, MARGARE M.
APPLICANT: Sunch, Victoria
APPLICANT: Sunch, Victoria
APPLICANT: Stone, Donna M.
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUNOR FILLS OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUNOR APPLICATION NUMBER: 60/01469
REIOR FILING DATE: 1996-04-01
PRIOR FILING DATE: 1996-09-23
REIOR APPLICATION NUMBER: 60/05932
REIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-10-10
PRIOR PLING DATE: 1997-10-10
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-24
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PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 10
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Similarity 100.0%; Pred. No. 5.3e-135;
45; Conservative 0; Mismatches 0;
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APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
APPLICANT: Proceeding Stermen
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERCE: B3630RICAL12
CURRENT PELLOR DATE: 2002-09-17
PRIOR PELLOR APPLICATION NUMBER: 06/05314
PRIOR APPLICATION NUMBER: 60/05314
PRIOR APPLICATION NUMBER: 60/063046
PRIOR APPLICATION NUMBER: 60/06507
PRIOR PELLOR DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/06507
PRIOR APPLICATION NUMBER: 60/06507
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08001
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/09
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Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0;
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121 ISKKOVFGLRREIPIPSTGSVEMAV 145
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Grimaldi, J. Christopher
Gurney, di, J. Christopher
Gurney, Austin
Smith, Victoria
Stephen, Jean-Phillippe
Watanbe, Colin
Wood, William
                                                                                                                                                                              Sequence 10, Application US/10245103 Publication No. US20030068778A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 PPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARPTYGGCYGNKNNPEEEQQCLESCRG 443
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION WINBER: 60/066772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NGS: 258
LENGTH: 529
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APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235R1L
CURRENT APPLICATION NUMBER: US/10/305,654
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 383
ERQ ID NO 42
LENGTH: 529
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                                                                                                                                                                                                                                                                                                           Length 529;
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Publication No. US20030224984A1
GENERAL INFORMATION:
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Gerber, Hans-Peter
Gerritsen, Mary B.
Goddard, Audrey
Godwekt, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
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Paoni, N. F.
Stephan, J-P.F.
Watanabe, C.K.
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                                                                                                                                                                                                t TYPE: PRT
CORGANISM: Homo sapiens
US-10-211-858-12
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ORGANISM: Homosapiens
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APPLICANT:
APPLICANT:
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APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Bang, Zemin
APPLICANT: Alang, Zemin
APPLICANT: Pong, Sherman
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILLS BAPPLICATION NUMBER: 10/10/245,107
CURRENT FILING DATE: 2002-09-16
FRIOR PILING DATE: 2002-09-16
FRIOR PILING DATE: 1997-10-24
FRIOR PILING DATE: 1997-10-24
FRIOR APPLICATION NUMBER: 60/06507
FRIOR APPLICATION NUMBER: 60/06507
FRIOR PILING DATE: 1998-03-27
FRIOR PILING DATE: 1998-03-27
FRIOR PILING DATE: 1998-03-27
FRIOR PILING DATE: 1998-06-02
FRIOR PILING DATE: 1998-06-04
FRIOR FILING DATE: 1998-06-04
FRIOR FILING DATE: 1998-06-05
FRIOR PILING DATE: 1998-06-05
FRIOR FILING DATE: 1998-06-05
FRIOR PILING DATE: 1998-06-05
FRIOR FILING DATE: 1998-06-05
FRIOR PILING DATE: 1998-06-05
FRIOR APPLICATION NUMBER: 60/09069
FRIOR PILING DATE: 1998-06-05
FRIOR APPLICATION NUMBER: 60/09069
FRIOR PILING DATE: 1998-06-05
FRIOR APPLICATION NUMBER: 60/09069
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                                                                                                                                         Eaton, Dan
Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Application US/10245107
To. US20030068779A1
                                                                                                                                                                                                                                                                                                                                                        Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
                                                                 GENERAL INFORMATION:
APPLICANT: Baker, Kevin
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US-10-245-107-10
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APPLICANT:
APPLICANT:
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Sequence 10, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan

US-10-245-143-10

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APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Charge, Sherman
APPLICANT: Charge, SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: 10/197942
PRIOR PLILNG DATE: 1002-109-16
PRIOR PLILNG DATE: 1097-109-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLILNG DATE: 1997-09-17
PRIOR PLILNG DATE: 1997-09-17
PRIOR PLILNG DATE: 1997-09-17
PRIOR PLILNG DATE: 1998-0-11-10
PRIOR PLILNG DATE: 1998-0-6-12
PRIOR PLILNG DATE: 1998-0-6-12
PRIOR PLILNG DATE: 1998-0-6-12
PRIOR PLILNG DATE: 1998-0-12
PRIOR PLILNG DATE: 1998-0-6-18
PRIOR PLILNG DATE: 1998-0-6-24
PRIOR PLILNG DATE: 1998-0-6-28
PRIOR PLILNG DATE: 1998-0-6-18
PRIOR PLILNG DATE: 1998-0-6-28
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Publication No. US20030068781A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watambe, Colin
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
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APPLICANT:
APPLICANT:
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US/10/245,851
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Publication No. US20030068783A1
GENERAL INFORMATION:
                  CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2002-09-
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Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-10-245-883-10
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LENGTH: 529
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Watange, Colin
APPLICANT: Watange, Colin
APPLICANT: Watange, Colin
APPLICANT: Alang, Zemin
APPLICANT: Alang, Zemin
APPLICANT: Pong, Sherman
APPLICANT: Pong, Sherman
APPLICANT: Pong, Sherman
ATTILE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3630R109 NOWER: US/10/245,771
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 0/053114
PRIOR APPLICATION NUMBER: 60/053114
PRIOR APPLICATION NUMBER: 60/053016
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PLILING DATE: 1998-05-22
PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDBAACEKYTSGFDELQRIH 383
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephen, Jean-Phillippe
Watanbe, Colin
Wood, William
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; Sequence 10, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baker, Caron, Dan
; APPLICANT: Playaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.4
Best Local Similarity 100.
Matches 145; Conservative
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ORGANISM: Homo Sapien
US-10-245-771-10
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324 MERRHPVCSGTCQPTQFRCSNGCCIDSPLECDDTPNCPDASDEAACEKYTSGFDELQRIH 383
PRIOR APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 10/197942
PRIOR PLING DATE: 1907-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-10-24
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-27
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
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70.4%; Score 145; DB 14; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT PAPALICATION NUMBER: US/10/245,883
CURRENT FILING DATE: 2002-09-16
PRIOR PRILICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
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Goddard, Audrey
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watambe, Colin
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120

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SAPELICANT: BARET, Kevin

APPLICANT: BARET, Kevin

APPLICANT: BARON, Man

APPLICANT: Flivanoff, Ella

APPLICANT: Flivanoff, Ella

APPLICANT: Gaddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Sachan, Jean-Phillippe

APPLICANT: Matanbe, Colin

APPLICANT: Matanbe, Colin

APPLICANT: Macanbe, Colin

APPLICANT: SCEPHAN, Jeann

APPLICANT: SCEPHAN, SECHETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P36.081C3

CURRENT FILING DATE: 2002-09-06

PRIOR FILING DATE: 10/197942

PRIOR FILING DATE: 1997-10-18

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065046

PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/06507

PRIOR FILING DATE: 1997-11-10
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PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065046
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-11-10
PRIOR PAPLICATION NUMBER: 60/079689
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/080801
PRIOR APPLICATION NUMBER: 60/080801
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
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PRIOR PILING DATE: 1908-06-25
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Best Local Similarity 100.0%; Pred. No. 5.3e-135;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps
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Publication No. US20030073188A1
GENERAL INFORMATION:
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US-10-245-883-10
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LENGTH: 529
TYPE: PRT
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PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/080601
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-27
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1999-03-10
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PRIOR PILING DATE: 1999-03-10
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PRIOR PILING DATE: 1999-03-13
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APPLICATION WINBER: 60/086478 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/087607

FILING DATE: 1998-03-27

us-09-935-390a-23.oll.rapb

PRIOR APPLICATION NUMBER: 60/16250
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-20
PRIOR PILING DATE: 1999-11-00-10
PRIOR PILING DATE: 2000-01-20
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PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-05
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/28099
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-13
PRIOR PILING DATE: 1999

PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
PRIOR APPLICATION NUMBER: 09/918585
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-08-06
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PRIOR APPLICATION NUMBER: 09/931836
PRIOR PILING DATE: 2001-08-16
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PRIOR PILING DATE: 2001-08-16
PRIOR PILING DATE: 2001-08-04
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PRIOR PILING DATE: 2001-01-06-04
PRIOR PILING DATE: 2001-01-06-04
PRIOR PILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-02-00
PRIOR PILING DATE: 2002-04-09

Query Match 70.4%; Score 145; DB 14; Length 529; Best Local Similarity 100.0%; Pred. No. 5.3e-135; Matches 145; Conservative 0; Mismatches 0; Indels

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1 MERRHPYCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDBLQRIH

121 ISKKDVPGLRRRIPIPSTGSVEMAV 145

444 ISKKDVFGLRRBIPIPSTGSVEMAV 468

Search completed: April 22, 2004, 10:32:27 Job time : 362 sec8

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This represents a human secreted protein. The specification provides secreted protein sequences (AAM63681 to AAM63699) encoded by the nucleic acid sequences shown in AAV43601 to AAV43619. The invention provides a method of identifying a secreted polypeptide which is modified by rough microsomes. The secreted proteins can be used in assays to determine biological activities, such as cytokine, cell proliferation, or cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; human; cell proliferation; cytokine activity; tissue growth; cellular differentiation; regeneration; activin; inhibin; chemotactic; haemostatic; thrombolytic; tumour inhibition; anti-inflammatory activity; blomarker.
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/note= "kunitz type serine protease inhibitor domain"
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WPI; 1998-348453/30.
N-PSDB; AAV43604.
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11-DEC-1997;
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(c) 1993 - 2004 Compugen Ltd.
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inhibin activity, chemotactic or chemokinetic activity, haemostatic or inhibin activity, chemotactic or chemokinetic activity, haemostatic or thrombolytic activity, receptor/ligand activity, tumour inhibition, or anti-inflammatory activity. The proteins can also be used as biomarkers, to identify tissues or cell types which express the proteins, or a stage-or disease-specific alteration in protein expression. They can be used in protein interaction assays, to identify ligands or binding proteins. Compounds which affect the biological activities of the secreted proteins or their ability to interact with specific ligands can be identified using the proteins in screening assays. The proteins and antibodies that contract with specific ligands can be identified using the proteins in screening assays. The proteins and antibodies that the protein compositions for diseases which may be associated with altered expression of these proteins. Fusion proteins comprising, or signal sequences or transmembrane domains of the proteins can be used to target other protein domains to cellular membrane or they can be secreted extracellularly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, protease associated protein, HPRAP, cancer, inflammation, anti-HTM, antiantemics, arcitateratiosclerotic, antiasthmatic, cytostatic, antiinflammatory, hepatotropic, antidiabetic, nephrotropic, antidot, antithyroid, immunosuppressive; thyromimetic, virucide, dermatological; neuroprotective, cardiant, osteopathic; antiathritic, antiparasitic, antipsociatic, uropathic, ophthalmological; antitheumatic, tranquiliser, vulnerary, antiulcer; immune disorder; gene therapy; HPRAP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH
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differentiation activities, tissue growth or regeneration, activin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MERRHPYCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protease associated protein HPRAP-2.
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100.0%;
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Best Local Similarity 100.
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 206 AA;
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                                                                                        (INCY-) INCYTE PHARM INC.
                                                                                              Tang YT,
                                                                                                      WPI; 2000-062147/05
                                                                          28-APR-1999;
                                                                                 01-MAY-1998;
                                                                   11-NOV-1999.
                                                                                              Hillman JL,
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181

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The present invention provides the protein and coding sequences of four human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3 and HPRAP-4, HARAP-4, HARAP-7, HARAP-4, HARAP-4
                                                     Novel human protease associated proteins used for, e.g. the diagnosis and prevention of cell proliferative and immune disorders.
                                                                                                                                                                Claim 1; Page; 75pp; English.
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69 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH Gaps . 100.0%; Score 206; DB 3; Length 348; 100.0%; Pred. No. 3.9e-198; ive 0; Mismatches 0; Indels (Best Local Similarity 100. Matches 206; Conservative Query Match ઠે

Sequence 348 AA;

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120
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                                                                                             ISKKOVFGLRREIPIPSTGSVEMAVAVFLVICIVVVVAILGYCFPKNQRKOFHGHFHEPP 180
PPSDKGHCVDLPDTGLCKES I PRWYYNPFSEHCARFTYGGCYGNKNNPEEEQQCLESCRG
                                                      PPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNNFBEEQQCLESCRG
                                                                                                                              263
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                                                                    203
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Human protease associated protein HPRAP-2. PIPASSTVSTIEDIEHLVYNHIIRPL 206 PTPASSTVSTTEDTEHLVYNHTTRPL 348 Ā AAO17718 standard; protein; 348 08-AUG-2002 (first entry) AA017718; 323 RESULT 3 ò 셤 **SEESEKEKEKK**

Human, protease associated protein; HPRAP, cancer; inflammation; anti-HIV; antianaemic; antiarteriosclerotic; antiasthmatic; cytostatic; antiflammatory; hepatotropic; antidiabetic; nephrotropic; antigout; antithyroid; immunosuppressive; thyromimetic; virucide; dermatologica; neuroprotective; cardiant; osteopathic; antiarthritic; antiparasitic;

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Novel human protease associated proteins used for, e.g. the diagnosis and prevention of cell proliferative and immune disorders.
antipsoriatic; uropathic; ophthalmological; antirheumatic; tranquiliser; vulnerary; antiulcer; immune disorder; gene therapy; HPRAP-2.
                                                                                                 Patterson C;
                                                                                                Guegler KJ,
                                                                                                 Corley NC,
                                                                                                                                             Disclosure, Page, 75pp; English.
                                                                                                 Lal P,
                                                         99WO-US009190.
                                                                                   (INCY-) INCYTE PHARM INC.
                                                                                                 Hillman JL, Tang YT,
                                                                                                             WPI; 2000-062147/05.
                   Homo sapiens.
                               W09957274-A1.
                                                         28-APR-1999;
                                            11-NOV-1999.
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The present invention provides the protein and coding sequences of four human protease associated proteins, designated HPRAP-1, HPRAP-2, HPRAP-3 and HPRAP-4, HPRAP-1, HPRAP-3, HPRAP-3 and HPRAP-4, HPRAP-1, HPRAP-1, HPRAP-3, HPRAP-3 and HPRAP-4, HPRAP-1, HPRAP-1, HPRAP-3, HPRAP-3 and HPRAP-4, HPRAP-1, HPRAP-3, HPRAP-3 and HPRAP-4, HPRAP-1, HPRAP-3, HPRAP-3 and HPRAP-4, HPRAP-3, HPRAP-3 and HPRAP-4, HPRAP-3, HPRAP-3, HPRAP-4, HPRAP-4, HPRAP-3, HPRAP-3, HPRAP-4, HPRAP-4, HPRAP-4, HPRAP-3, HPRAP-4, HPRAP-4, HPRAP-3, HPRAP-4, HPRAP-3, HPRAP-4, HPRAP-4, HPRAP-3, HPRAP-4, HPRAP-4, HPRAP-3, HPRAP-4, HPRAP-3, HPRAP-4, HPRAP-3, HPRAP-4, HPRAP-4, HPRAP-3, HPRAP-4, HPRAP-4

Sequence 348 AA;

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MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 202
                                                                                                                            PPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARPTYGGCYGNKNNFEEEQQCLESCRG 120
                                                                                                                                                                                           ISKKDVFGLRREIPIPSTGSVEMAVAVFLVICIVVVVALLGYCFFKNQRKDFHGHHHPP 180
                                                                                                                                                                                                        203 FPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNNFEEBGQCLESCRG 262
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                                                                1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDBAACEKYTSGFDBLQRIH
                                 Gaps
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100.0%; Score 206; DB 3; Length 348; 100.0%; Pred. No. 3.9e-198;
                                0; Indels
                                0; Mismatches
                                Matches 206; Conservative
               Similarity
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PTPASSTVSTTEDTEHLVYNHTTRPL 206

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121 ISKKDVFGLRREIPIPSTGSVENAVAVFLVICIVVVVAILGYCFFKNQRKDFHGHHHPP 180

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428 ISKKOVFGLRREIPIPSTGSVEMAVAVFLVICIVVVVAILGYCFFRNQRKDFHGHHFHPP

487

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368 PPSDKGHCYDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGWKNNFEEEQQCLESCRG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an inhibitor of the protease activity of hepatocyte growth factor (HGF) activator (HGFA), which has a molecular weight of about 40 kD when determined by SDS-PAGE. The inhibitor, which was isolated from the human cancer cell line MKN45, can be used as an in vivo or in vitro regulatory factor for HGF or HGFA. It can also be used to raise antibodies, useful in kinetic studies of the inhibitor, or as
                                                                                                                                                                                                       Inhibition; inhibitor; proteage; hepatocyte; growth factor; activation; activator; human; cancer; cell line; MKN45; regulation; regulator; antibody; kinetic study; assay standard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hepatocyte growth factor activator inhibitor and DNA - regulates hepatocyte growth factor and/or HGF activator in vivo or in vitro, and are used in kinetic studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PPSDKGHCVDLPDTGLCKBSIPRWYYNPPSEHCARFTYGGCYGNKNNFBBBQQCLESCRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MERRHPYCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAGEKYTSGFDELQRIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miyazawa
                                                                                                                                                                           Hepatocyte growth factor activator inhibitor.
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1. .35
/label=_sig_peptide
                                                                                                                                                                                                                                                                                                                                        36. .513
/label= mat_peptide
                                                                                                                                                                                                                                                                                               Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 28-30; 38pp; English.
                                                                                       513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MITU ) MITSUBISHI CHEM CORP.
                                                                                       AAW27368 standard; protein;
                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 1997-147516/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 513 AA;
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                                                                                                                                                                                                                                                                    Ношо варієль.
                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-1995;
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                                                                                                                                                21-NOV-1997
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                                                                                                                  AAW27368;
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                                                                           AAW27368
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ISKXDVPGLRREI PIPSTGSVEMAVAVFLVICIVVVVAILGYCPPKNQRKDFHGHHPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a preventive and/or treating agent for the diseases caused by the exasperation of activity of protease of plasma kallikrein, plasmin, urokinase and trypsin. The agent contains a protein, HAI-1 which has the following properties, M.W. of ca. 40,000 to 57,000 balton by SDS-PAGE and an activity of inhibiting protease activity of hepatocyte growth factor (HGF) activator. The HGF inhibiting activity of the protein is specific. HAI-1 shows a high inhibiting activity of plasmin, trypsin, HGF activator and plasma kallikrein but substantially no inhibiting activity on thrombin. This sequence represents the human HAI-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 60
                                                                                                                                                                                                                                  Hepatocyte growth factor; HAI-1; HGF inhibiting factor; human; plasmin; treatment; prevention; protease activity; plasma; urokinase; trypsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A preventive and/or treating agent for the diseases caused by the exasperation of activity of protease - inhibits protease activity hepatocyte growth factor (HGP) activator.
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/label= signal_peptide
36. .513
PTPASSTVSTTEDTEHLVYNHTTRPL
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                                                                                                            AAW92653 standard, protein; 513
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/label= HAI-1
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                                                                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-186215/16.
N-PSDB; AAX02200.
                                                                                                                                                                                                         Human HAI-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              JP11035480-A.
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                                                                                                                                                                                                                                                                                    Homo sapiens
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   181
                                 488
                                                                                                                                         AAW92653;
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Human; protein modification and maintenance molecule; PMMM; cancer; cell proliferation disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; inflammatory disorder; AlDS; developmental disorder; hypothyroidism; cushing's syndrome; gastrointestinal disorder; pypothyroidism; infection; cytostatic, antiarieriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary; antiinflammatory; thyromimetic.
                                                                                                                 Human protein modification and maintenance molecule-23 (PMMM-23).
 206
                  513
ABU92043 standard; protein; 487 AA
                                                                                                                                                                                                                                                                                               12-OCT-2001; 2001US-0329689P.
25-OCT-2001; 2001US-0335703P.
09-NOV-2001; 2001US-0348887P.
28-NOV-2001; 2001US-0334145P.
06-DEC-2001; 2001US-0337411P.
                                                                                                                                                                                                                                                                              11-OCT-2002; 2002WO-US032850
                                                                                                    (first entry)
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                                                                                                                                                                                                                          Homo sapiens.
                                                                                                   15-JUL-2003
                                                                                                                                                                                                                                                            17-APR-2003
                                                                                  ABU92043;
                                                         ABU92043
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New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or Ä Ramkumar J, Gorvad AB, Baughn MR, Emerling BM, Yang J, Lee SY; Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX; Sprague WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AB, Yue J Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D; Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W; WPI; 2003-430274/40. N-PSDB; ACA92438. infections.

(INCY-) INCYTE GENOMICS INC.

Claim 1; Page 263-264; 311pp; English.

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The present invention relates to the isolation of human protein modification and maintenance molecules (PAMM), and the polymucleotide modification and maintenance molecules (PAMM), and the polymucleotide sequences encoding them. A total of 40 PAMM polypeptides (designated PAMM-1 resquences encoding them. A total of 40 PAMM polymucleotides are disclosed. The sequences of the invention are useful for disapposing a condition of disease associated with the expression of PAMM in a subject, preparing a polythonal or monoclonal antibody, and polymucleotides. The disease or conditions associated with decreased expression or overexpression of PAMM are cell proliferation disorders (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. allergies), developmental disorders (e.g. hypothyroidism, Cabhing's allergies) asstrointestinal disorders (e.g. hypothyroidism, Cabhing's PAMMM polypeptides or their fragments are useful in screening compounds for effectiveness as agonists or antagonists of the polypeptides, or in

us-09-935-390a-23.oli.rag

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The present sequence is that of novel human immunomodulator PR0256 (UNQ223), as deduced from cDNA (see AAF30055) isolated from a placental tissue library. PR0256 (See R. Ma., p16.22) shows sequence homology to human bikunin protein, suggesting protease-inhibitor activity. The invention proteins proteins of proteins (see AAF30050.62) encoding novel human PR0 provides polymucleotides (see AAF30050.62) encoding novel human PR0 comprising these proteins or their agonists are useful for increasing the proteins of inflammatory calls into a tissue of a mammal; stimularing comprising an immune response, or increasing the proliferation of T-1 (Inflammatory propagate) or increasing the proliferation of T-2 (Inflammatory propagate) or increasing the proliferation of T-3 (Inflammatory myopathy, Siogrefur is selected from a propagate in the proliferation of the proliferation of thromborytopaenia, autoimmune haemolytic anaemia, autoimmune thromborytopaenia, thyroiditis, diabetes mellitus, immune-adiated diseases (such as multiple sclerosis), autoimmune conclusis, granulomatous conclusis, sacrosidosis, primary biliary cirrhosis, granulomatous conclusis and Crohn's diseases (such as multiple sclerosis), autoimmune-mediated skind seases (such as bullous skin disease, (autoimmune-mediated skind seases (such as bullous skin diseases (autoimmune-mediated skind as graft relegation), immunologic diseases (the lung and transplantation cartive diseases (autoimmune-mediated skind as graft relegation), allergic rhinities, atogic dermatities, allergic relegation of disagnosing these discrets comprise detecting the level of expression of the PRO gene. Also claimed are method of indentifying a compound capable of inhibiting the proliferation of artivity of the PRO polypoppide, verificanti
Peptide
                                                                                                                                                                                 Domain
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                                                                                                                                                    TSGPDELQRIHPPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNNPE 109
                                                                                                                                                                  331 TSGFDELQRIHFPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNNFE 390
                                                                                                                                                                                                            110 BEQQCLESCRGISKKDVFGLRREIPIPSTGSVEMAVAFLVICIVVVVALLGYCFFKNQR 169
                                                                                                                                                                                                                            PRO256; UNQ223; human; immune disease; autoimmune disease; antirheumatic;
altering the expression of the target polymucleotide and compounds that specifically bind to, or modulate the activity of the polypeptide. ABU92021-ABU92060 represent the human PMVM polypeptides of the invention
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protein motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipatoriatic; antiasthmatic; antiallergic; immunostimulant; protease-inhibitor.
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                                                                                         Length 487;
                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                       KUPHCHHHHPPPTPASSTVSTTEDTEHLVYNHTTRPL 206
                                                                                                                                                                                                                                                                                       KOFHGHIHIPPPPTPASSTVSTTBDTEHLVYNHTTRDL 487
                                                                                         Score 157; DB 6; Le
; Pred. No. 8.3e-149;
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note= "N-myristoylation site"
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313. .319
/note= "N-myristoylation site"
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/note= "N-myristoylation site"
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/note= "N-myristoylation site"
                                                                                       76.2%; Score 157; DE ilarity 100.0%; Pred. No. 8.3 Conservative 0; Mismatches
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/label= Signal_peptide
29. .35
/note= "N-myristoylatic
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label= Mature_protein
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/note= "N
66. .70
/note= "A
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                                                            Sequence 487 AA;
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Best Local
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"low density lipoprotein class A domain protein
                                           /note= "pancreatic trypsin inhibitor (Kunitz) family protein motif"
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Pitti RM, Tumas
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Mark MR, Marsters SA,
                                                                                                                                           /note= "N-myristoylation site"
426. .432
                                                                                                                                                                                                                                /note= "transmembrane domain"
523. .527
/note= "Asn is N-glycosylated"
                                                                                                                                                                                            "M-myristoylation site"
                                                                                             422. .428
/note= "M-myristoylation site"
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                                                                                                                                                                                          /note= '466. .48
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Gurney AL, Hillan KJ,
Watanabe CK, Wood WI;
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N-PSDB; AAF30055.
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                                                                                                                    FPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNNFEEEQQCLESCRG 443
                                                                                        324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDTPNCPDASDEAACEKTTSGPDELQRIH 383
                                                                                                                                                                                                                                                                                    Human; PRO256 protein; cardiovascular; endothelial; angiogenic disorder; cardiac hypertrophy; trauma; cardiant; age-related manular degeneration; gene therapy; angiogenesis; protease activity; hepatocyte growth factor; peripheral vascular disease, hepatic; renal injury; nephrotropic; tumour; restinosis; tranquillizer; vulnerary; cytostatic; hepatotropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Human mature hepatocyte growth factor activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Pancreatic trypsin inhibitor family signature"
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                                                                       1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDBAACBKYTSGFDBLQRIH
                                                      Gaps
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                                   Length 529;
                                  70.4%; Score 145; DB 4; Length 52
100.0%; Pred. No. 1e-136;
ive 0; Mismatches 0; Indels
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193. .199
/note= "Cell attachment sequence"
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/note= "Asn is N-glycosylated"
278. .298
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/note= "N-myristoylation site"
285. 291
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/label= Signal_peptide
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                                                                                                                                                        Location/Qualifiers
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281. .287
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                                            Local Similarity 100.4
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/note= "N
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lymphocytes using PRO256
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                                                                                                                                                                                                                                                                  Human PRO256 protein.
                 Sequence 529 AA;
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The present invention relates to PRO256 or its agonist/antagonist may be used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, especially a human with cardiac hypertrophy, trauma, a type of tumour or age-related macular degeneration. PRO256 may be administered together with a cardiovascular, endothelial, or angiogenic agent, a chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent. PRO256 may also be used to treat the disorders above, preferably through administration via ex vivo gene therapy. PRO356 or its agonist may be used to inhibit endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor. Whereas an antagonist of PRO256 may be used to stimulate endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor. Stimulation or inhibition of the protease activity of a hepatocyte growth factor. Stimulation or inhibition of the protease activity of a hepatocyte growth factor is preferably carried out where a mammal has a cardiovascular, endothelial, or angiogenic disorder selected from peripheral vascular disease, hepatic or remal injury or a restinosis disorder. The present sequence is human hepatocyte growth factor activator inhibitor, PRO256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated polypeptide designated PRO256 useful for treating cardiovascular, endothelial, or angiogenic disorder.
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                                    "N-myristoylation site"
                                                                                              "N-myristoylation site"
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/label= Transmembrane_domain
523. .527
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ID AAU86133 standard; protein; 529 AA.
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15-MAR-2000; 2000WO-US006884.
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Matches 145, Conservative
                                    /note=
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PPSDKGHCVDLPDTGLCKESIPRMYYNPFSEHCARFTYGGCYGNKNNFBEEDQCLESCRG 120
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17-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides and the polymoclectide sequences encoding them. The PRO polypeptides, agonists, antagomists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and iymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoalic disorders, inflamatory, immune and angiogenic disorders. The polymucleotide sequences are also useful in gene therapy, AAU86122 represent the human PRO polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders.
                                                                                                   Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
letkeemia; neuronal disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention relates to the isolation of novel human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillan KJ;
Stone DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.4%; Score 145; DB 5; Length 529; 100.0%; Pred. No. 1e-136; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL,
Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, H
Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 61; Fig 12; 302pp; English.
                                                                                                                                                                                                                                                                                 99WO-US005028.
99US-0123972P.
99US-0133459P.
99US-0140650P.
99US-0140653P.
99US-0146658P.
99US-014568B.
99US-014568B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US028301
                                                 15-JUL-2002 (first entry)
                                                                            Human PRO256 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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                                                                                                                                                                                                     WO200153486-A1.
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05-JAN-2000;
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     20-JUL-1999;
26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
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30-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-1999)
                                                                                                                                                                                                                                                                                                 11-MAR-1999
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                                                                                                                                                                                                                               26-JUL-2001
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                        AAU86133;
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384 PPSDKGHCVDLPDTGLCKESIPRWYNPFSEHCARFTYGGCYGNKNNFEEEQQCLESCRG 443
                                                                                                                                                                                                Human; anglogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; spene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; thebusatoid arthritis; mycardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                                                                                                                                                                               Human PRO256 protein sequence SEQ ID NO:42.
                                             444 ISKKDVPGLRREIPIPSTGSVEMAV 468
                                 121 ISKKDVFGLRREIPIPSTGSVEMAV
                                                                                                               ABB84837 standard; protein; 529 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US020710.
2000US-0222695P.
2000US-00643657.
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2000US-00665350.
2000US-0242922P.
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2000WO-US0330952.
2000WO-US033673.
2000WO-US033678.
2000WO-US034678.
2001WS-00747259.
2001US-007467609.
2001WS-0076666.
2001WS-00806666.
2001US-00808689.
2001US-00808689.
2001US-00808689.
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2000US-0230978P.
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                                                                                                                                                          (first entry)
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(GETH) GENENTECH

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0; Gaps

324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLBCDDTPNCPDASDEAACEKYTSGFDELQRIH 383

MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 60

Local Similarity nes 145; Conservative

Matches

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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to all ABB85003. The PRO proteins and polymucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polymucleotides, proteins, agonists and antagonists are useful for treating or diagnosing cardiac hypertrophy, traums, cancer, age-related macular degeneration, atherosclerosis, hypertension, atterial restences, rheumatoid arthritis, angina, myccardial inferctions, thrombophebitis, lymphangitis, tumour angiogenesis (such as breast cartinoma and liver cardinoma) and wound healing. The PRO polymucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88159 to ABL8825, represent primers and probes used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNNFEEEQQCLESCRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEXYTSGFDBLQRIH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO; secreted protein; transmembrane protein; genetic disorder;
                  Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                    One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.4%; Score 145; DB 5; Length 529; Best Local Similarity 100.0%; Pred. No. 1e-136; Matches 145; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 ISKKDVFGLRREIPIPSTGSVEMAV 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG34034 standard; protein; 529 AA.
                                                                                                                                                                                                                                  Claim 11; Fig 42; 565pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000; 2000US-0229896P.
05-SEP-2000; 2000US-023651P.
22-SEP-2000; 2000US-0235147P.
10-NOV-2000; 2000MO-US030873.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Pro peptide #5.
                                                                                            WPI; 2002-090516/12.
N-PSDB; ABL88092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 529 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200224888-A2.
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This invention relates to the cDNA and protein sequences of novel secreted and transmembrane polypeptides PRO polypeptides. The invention also comprises a method for producing the proteins of the invention by recombinant means and antibodies specific for the protein of the invention by recombinant means and antibodies specific for the protein of the invention. The antibody may be used for detecting the PRO proteins of the invention and may be used to modify their activity. polymucleotides may be used as hybridisation probes for a cDNA library to isolate the full-bength PRO cDNA or to isolate other CDNAs, to construct hybridisation probes for mapping the gene which encodes that PRO and for genetic analysis of individuals with genetic disorders, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knock-out animals which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides are useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect oversappession on PRO polypeptides in cancerous tumnurs and for screening for differentially expressed genes using microarray technology. The present sequence represents a human PRO protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptides and polynucleotides encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 MERRHPVCSGTCQPIQFRCSNGCCIDSFLECDTPNCPDASDEAACEKYTSGFDELQRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MERRHPVCSGTCQPTQFRCSNGCC1DSFLECDDTPNCPDASDBAACEKYTSGFDELQRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                             Grimaldi JC;
Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.4%; Score 145; DB 5; Length 529; 100.0%; Pred. No. 1e-136; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Eaton DL, Filvaroff E, Goddard A, Smith V, Stephan J, Watanabe CK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 10; 218pp; English.
                                                                                                                   2001MO-US006520
2001US-0274399P.
2001US-0280982P.
2001US-0282139P.
2001US-0282199P.
                                 2001US-0261939P.
2001US-0262150P.
2001US-0264395P.
2001US-0266421P.
2001US-0267623P.
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2001WO-US019692
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Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-362426/39.
N-PSDB; ABK69965.
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                                 16-JAN-2001;
16-JAN-2001;
25-JAN-2001;
02-FEB-2001;
09-FEB-2001;
                                                                                                                       28-FEB-2001;
09-MAR-2001;
03-APR-2001;
                                                                                                                                                                              04-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                 Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Paoni NF;

Goddard A; SA, Pan J,

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Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; tumour necrosis factor-alpha; TWF-alpha; blood; chondrocyte cell; tumour; adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer; microvascular endothelial cell; endothelial cell tube formation; sporte-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarention, thromopolibeliis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MERRHPYCSGTCOPTOFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELORIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FPSDXGHCVDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNVFBEEQQCLESCRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 FPSDKGHCVDLPDTGLCKGSIPRWYNPFSEHCARFTYGGCYGNKNNPEBEQQCLESCRG
                                                                                                                                 One hundred and eighty seven mucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                        70.4%; Score 145; DB 5; Length 529; 100.0%; Pred. No. 1e-136; ive 0; Mismatches 0; Indels
                                     Baker KP, Ferrara N, Gerber H, Gerritsen ME, G
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA,
Stephan JF, Watanabe CK, Williams PM, Wood WI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA01278 standard; protein; 529 AA.
                                                                                                                                                                                            Claim 11, Fig 42; 567pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-2001; 2001US-0290589P.
29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.4
Best Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide #5
(WILL/) WILLIAMS P M. (WOOD/) WOOD W I.
                                                                                              WPI; 2002-171999/22
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                                                                                                             N-PSDB; ABL95581
                                                                                                                                                                                                                                                                                                                                                  Sequence 529 AA;
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                                                                                                                                     Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic.
                                                                                                                Human angiogenesis related protein PRO256 SEQ ID NO: 42.
                                  ABB95443 standard; protein; 529 AA
                                                                                                                                                                                                                                                                                                                        20-JUL-2000; 2000US-0219556P.
25-JUL-2000; 2000US-0220664P.
28-JUL-2000; 2000US-0220664P.
28-JUL-2000; 2000US-0222655P.
17-AUG-2000; 2000US-0222655P.
23-AUG-2000; 2000US-00643657.
23-AUG-2000; 2000US-00643657.
24-AUG-2000; 2000WS-030374P.
18-SEP-2000; 2000WS-030374P.
18-SEP-2000; 2000WS-030374P.
18-SEP-2000; 2000WS-030374P.
19-SEP-2000; 2000WS-0303752.
10-NOV-2000; 2000WS-0303752.
10-NOV-2000; 2000WS-0303752.
10-NOV-2000; 2000WS-0303752.
10-NOV-2000; 2000WS-0303752.
22-JAN-2001; 2000WS-0303752.
22-JAN-2001; 2001WS-00767669.
22-MAR-2001; 2001WS-0086669.
22-MAR-2001; 2001WS-00854280.
22-MAY-2001; 2001WS-00854280.
25-MAY-2001; 2001WS-00854280.
25-MAY-2001; 2001WS-00856039.
25-MAY-2001; 2001WS-00856039.
25-MAY-2001; 2001WS-00856039.
25-MAY-2001; 2001WS-00851744.
01-UTN-2001; 2001WS-008517092.
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                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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GERRITSEN M.E.
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STEPHAN J F.
WATANABE C K.
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FERRARA N.
                                                                                                                                                                                                                                             WO200208284-A2
                                                                                                                                                                                                                    Homo варіепв.
                                                                                       19-JUL-2002
                                                                                                                                                                                                                                                                         31-JAN-2002
                                                              ABB95443;
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(GETH ) GENENTECH INC
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Grimaldi JC; Wood WI, Zhang Z; Filvaroff E, Goddard A, (Stephan JP, Watanabe CK, Baker KP, Eaton DL, Gurney AL, Smith V, Fong S;

WPI; 2003-625484/59. N-PSDB; ADA01277.

Novel isolated PR01313, PR020080 or PR021383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, and PR05018 polypeptide useful for stimulating proliferation of chondrocyte

Claim 11; Fig 10; 307pp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polymucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TWP-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a memmal (e.g. adrena), lung, colon, breast, prostate, rectal, cervical and liver tumours). The proliferation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. Including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in penerating either transgenic animals or knock-out animals which are useful in the development and streeming of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microwascular endothelial cells, for inducing endothelial cell cantilage defects, osteobatrhitis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

Sequence 529 AA;

ö 324 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACBKYTSGFDELQRIH 383 61 PPSDKGHCVDLPOTGLCKESIPRMYYNPPSEHCARPTYGGCYGNKNNFEEEQQCLESCRG 120 384 FPSDKGHCVDLPDFGLCKESIPRWYNPFSEHCARFTYGGCYGNRONFEEEQQCLESCRG 443 1 MERRHPVCSGTCOPTOFRCSNGCCIDSFLECDDTPNCPDASDEAACEXYTSGFDELQRIH 60 0; Gaps 70.4%; Score 145; DB 6; Length 529; 100.0%; Pred. No. 1e-136; Live 0; Mismatches 0; Indels 121 ISKKDVFGLRREIPIPSTGSVEMAV 145 Best Local Similarity 100. Matches 145; Conservative Query Match 셤 d ઠે ઠે ò

RESULT 14

ADA43707 standard; protein; 529 AA. 20-NOV-2003 (first entry) ADA43707;

Human secreted/transmembrane polypeptide PRO256.

Human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.

US2003064474-A1. Homo sapiens.

03-APR-2003.

16-SEP-2002; 2002US-00245859.

29-AUG-2001; 2001WO-US027099. 18-JUL-2002; 2002US-00197942.

(GBTH) GENENTECH INC

Filvaroff E, Goddard A, Grimaldi JC; Stephan JP, Watanabe CK, Wood WI, Zhang Z; Eaton DL, Smith V, Baker KP, Ś Surney Fong

WPI; 2003-605867/57. N-PSDB; ADA43706. New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or PRO21383, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 11; Fig 10; 308pp; English.

The interaction relates to an insolated secreted. Transmenaries (FRO) to polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the 57 amino acid sequences given in specification, or to a nucleic acid deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO in specification, or a sequence having at least 80% identity to PRO in specification, or a sequence having at least 80% identity to PRO with or without its associated signal peptide. Also included are vectors, transformed host calls, anti-PRO antibodies, the nucleic acids encoding PRO, PRO tusion procteins, inducing endothelial call tube formation (by administering PRO281, PRO1560, PRO189, PRO4499, PRO4499, PRO6800, PRO150175, PRO12107, PRO22031 or PRO481274 polypeptide or its agonist) and oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4497 and PRO6006 and PRO2133 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for inhibiting endothelial cells. PRO 2019 PRO497 and PRO6006 PRO189, PRO6009, PRO6009, PRO499, PRO6009, PRO6009, PRO1809, PRO6009, PRO1809, PRO6009, The invention relates to an isolated secreted/transmembrane (PRO)

Sequence 529 AA;

0; Gaps Query Match 70.4%; Score 145; DB 6; Length 529; Best Local Similarity 100.0%; Pred. No. 1e-136; Matches 145; Conservative 0; Mismatches 0; Indels

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443 61 PPSDKGHCVDLPDTGLCKES1PRWYNPPSEHCARFTYGGCYGNKNNFEEEQQCLESCRG 120 PPSDKGHCVDLPDTGLCKESIPRWYNPFSBHCARFTYGGCYGNKNNFEBBQQCLESCRG

The invention relates to an isolated secreted/transmembrane (PRO)

CO polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the mucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the mucleic acids encoding PRO, PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering process). PROSO93, Or PROJO275, PROSO93, Or PROSO93, or PROSO93, or enclanded are vectoride proceinde probe derived from any one of the above nucleotide sequences. PROSO133 or propertide is useful for stimulating the proliferation of proliferation or differentiation of chondrocyte cells. PROSO133, PROSO080 cc multiple polypeptides are useful for stimulating the proliferation of human corovascular endothelial cells. PROSO31, PROSO93, PROSO06 colon, breast, prostate, rectal, kidney and liver. PROS31, PROSO03 colon, breast, prostate, rectal, kidney and liver. PROS31, PROSO93 and PROSO3474 polypeptides are useful for inducing endothelial cell tube for proliferation of human colon, breast, prostate, rectal, kidney and liver. PROS31, PROSO933 and PROSO34274 polypeptides are useful for inducing endothelial cell tube for maticoance of tumour in a mammal including the proliferation of medicament for treating a condition responsive to PRO polypeptide. The antibody are useful in the preparation of medicament for treating a condition responsive to PRO polypeptide. The New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or PRO21383 useful for stimulating the proliferation or differentiation of chondrocyte cells and detecting the presence of a tumor in a mammal. Ŋ Human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular madothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine. Grimaldi JC; Wood WI, Zhang Human secreted/transmembrane polypeptide PRO256. Goddard A, Watanabe CK, 121 ISKKDVFGLRREIPIPSTGSVEMAV 145 ы́ Ź Filvaroff E, Stephan JP, English ADA43475 standard, protein; 529 04-APR-2001; 2001US-0282199P. 29-AUG-2001; 2001WO-US027099. 18-JUL-2002; 2002US-00197942. 18-SEP-2002; 2002US-00246210. (first entry) Claim 11; Fig 10; 307pp; (GETH) GENENTECH INC. KP, Eaton DL, AL, Smith V, WPI; 2003-743814/70. N-PSDB; ADA43474. US2003073196-A1. Homo sapiens 20-NOV-2003 17-APR-2003 Baker KP, ADA43475; 444 Gurney A Fong S; Fong ADA43475 셤 ò

ö as a m of 383 61 PPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNNPEEEQQCLESCRG 120 443 nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence represents a PRO protein. 9 1 MERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 384 PPSDKGHCVDLPDTGLCKGSIPRWYNPFSEHCARFTYGGCYGNNNPEBEDQQCLESCRG 0; Gaps oligonucleotide probes are useful for isolating genomic and cDNA Length 529; Query Match 70.4%; Score 145; DB 6; Length 52 Best Local Similarity 100.0%; Pred. No. 1e-136; Matches 145; Conservative 0; Mismatches 0; Indels 444 ISKKDVPGLRREIPIPSTGSVEMAV 468 121 ISKKDVFGLRREIPIPSTGSVEMAV 145 completed: April 22, 2004, 10:23:38 te : 72 secs Sequence 529 AA; Job time Search 888888888 윱 셤 ठे ò ò

Perfect score:

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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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    Faraday Avenue Genoscope sequence ID : CSODI009AB06NP1.

Location/Qualifiers
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Genoscope - Centrer National de Sequencage
BP 191 91006 EVRY cedex - France
BRail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Elibrary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1083CC11NP1&cluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
Feng Liang Email : fliang@lifetech.com invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1083CC11NP1.
Location/Qualifiers
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1267 TCCATGCTGTGCGCCCAGGGCTGGGAAGAACTTCCCTGTGTAGTTTGTGCTGTAAAG 208
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Scor V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Butheria; Primates; Catarrhini; Hoi
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Trill-length cDNA libraries and normalization
Unpublished (2001)
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EX360438 1073 bp mRNA linear EST 05-MAX-2003
CON EX360438 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSDIO707A20 3-PRIME, mRNA sequence.

EX360438 I GI:30378436
SET.
Homo sapiens (human)
ESM Homo sapiens (human)
ESM Homo sapiens (human)
ESM Homo sapiens
ENARAYOFG; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
ELI,W.B. Gruber; C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
LU Unpublished (2001) Contact: Genoscope
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Inbrary was constructed by Life Technologies, a division of
Inbrary was constructed by Life Technologies, a division of
Introduce information about this cluster, see
Introduce information about this cluster, see
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Awence Genoscope sequence ID : CSODIO70BA10NP1.
Location/Qualifiers
Intro ņ 822 975 522 916 582 642 797 702 737 762 677 617 857 > /organism="Homo sapiens"
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1101 GCSGSKGACYKCCAGACAMAG--AYTYKSAAAGAGAGCATCCCCGGTTGKTATTAMAACC 1044
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                                                                                                                             /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="let strand cDNA was primed with a Not1-01igo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pGMVSPORT 6 vector. Library was normalized."
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Avenue Genoscope sequence ID : CSODIO70CE12NP1 Location/Qualifiers
                                                                                                                                                                                                                                                                             63.9%; Score 961, DB 13; Length 1192;
.larity 93.9%; Pred. No. 1.6e-152;
Conservative 25; Mismatches 27; Indels 15.
                                                      /organism="Homo sapiens"
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                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI070YJ23"
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Matches 1026; Conserv
    Faraday
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BX381856 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODIO704723 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                               TGTCAGACCCTGGAGGCCCCCAACCCTGTCCTCCCGAGCTCCTTCCATGCTGTGCGCCC 1182
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1 (bases 1 to 1192)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length conta libraries and normalization
Unpublished (2001)
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                CAGAAGTACCAGACTAGATGGACCTGCCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTG
                                  CAGCTAAGCTCACGTCCTGAGAAAGCTCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGC
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                                                                                       CTOTTTCCCAGGCCCACTGTGCCTCAGAGACCAGGCTCCAGCCCCTCTTGGAGAAGTCT
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Contact: Genoscope and attional de Sequencage
Genoscope. Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: Seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOBSOBGE03QP1&cluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fullibrgth.invitrogen.com/ InvitroGen Corporation 1600
Fareday Avenue Genoscope sequence ID : CSOBE008CB03QP1.
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1244118 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE008YD05
5-PRIME, mRNA sequence.
AL542118
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                           909 GAGACCAGGGCCCCCTTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 968
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1 (Dases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

W.B., Gruber, C., Jessee, J. and Polayes, D.

Unpublished (2001)

On Peb 15, 2001 this sequence version replaced gi:12873845.
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Homo sapiens
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                                                   BX344105 1026 bp mRNA linear EST 02-MAY-2003 13344105 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLODE CSODIO57XA06 3-PRIME, mRNA sequence.
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/mol types=markA*

/db Aref="taxon:9666"

/clone="CSODIO571A06"

/clone="CSODIO57TA06"

/clone="type="PlackTRNTA COT 25-NORMALIZED"

/clone lib="Homo sapiens PlackTRTA COT 25-NORMALIZED"

/note="lst strand cDNA was primed with a NotI-oligo(dT)

primer: Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EORR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1026)
Li,W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDha, libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BFMail: segrefagenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
http://www.genoscope.cns.fr/
cgi-bin/cluster.ogi/seeq-cStAIO15ZA04NP1&cluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faradday Avenue Genoscope sequence ID : CSIAIO15ZA04NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           947 ACTTTGAGGAAGAAGAGCAGCAGTGCCTCGAGTCTTGTCSC-GCATCTCCAAGAAGGATGTGT
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                                                                                                                                                 BX344105.1 GI:30344237
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Homo sapiens
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RESULT 6
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DEFINITION
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TITLE
JOURNAL
COMMENT
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Contact: Genoscope

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 9106 EVRY cedex - France

BRMail: Beqrefegenoscope.cns.fr, Web: www.genoscope.cns.fr

Inbrary was constructed by Life Technologies, a division of

Inbrary was constructed by Life Technologies, a division of

Inbrary was constructed by Life Technologies, a division of

Introperation about this cluster, see

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi?seq=Cs0b1083CD10NP1ccluster=7854.fr Contact:

cgi-bin/Cluster_cgi?seq=Cs0b1083CD10NP1ccluster=7854.fr Contact:

Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invirrogen.com/ InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CS0D1083CD10NP1.
                                                                            1412
                                                                                                                                                                                                                                                                                                                                                                       BX340192 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO83YH19 3-PRIME, mRNA sequence.
CICIAICCICICITCCICTICCCCCAAGAITGAGCICICTGGCCCTTGAICAGCCCCACCC 1352
                                                                                                                                                     933
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1 (Dases 1 to 974)

1 (Liv.B., Catuber, C., Jessee, J. and Polayes, D.

Full-length cDNA, libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/do xref="texon:0606"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/clone_lis strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                            TGGCCTAGACCAGCAGAGAGCCAGGAGAAGCTCAGCTGCATTCCGCAGCCCCCACCCC
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llarity 98.7%; Pred. No. 4.1e-148;
Conservative 3; Mismatches 8; Indels 2
                                                                                                                                                                                                                                      1473 AAAAAAAAAAAAAAAAA 1492
                                                                                                                                                                                                                                                                           1052 AAAAAAAAAAAAAAA 1071
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BX340192.1 GI:30341878
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Homo sapiens
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nes 960; Conserv
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        1293
                                                                                   1353
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VERSION
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BX340192/c
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                    /mol type="mewa" wartene
/db xref="mewa"
/db xref="taxon.9606"
/clone="CSODE008YD05"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dRI) primer. Five prime end enriched,
watch a NotI-oligo(dRI) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
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                                                                                                                                                                                                                                                                                                                                                                                 AAGCAGGCTGCGGTCCGGGAATTCCCGGGATGGAAGAGCAGCAGTGCCTCGAGTCTT
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                                    CACCACCCACCCACCCACCCCTGCCAGCTCCACTCCCACTACCCAGGAGCACGGAGG
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BX360812 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI075YN13 3-PRIME, mRNA sequence. Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi, Mammallai, Eutheria, Primates; Catarrhini, Hominidae, Homo. 1 (bases 1 to 1201) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. BX360812 BX360812.1 GI:30366469 Homo sapiens (human) Homo sapiens BX360812/c LOCUS DEFINITION ORGANISM ACCESSION REFERENCE AUTHORS VERSION KEYWORDS SOURCE

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541 1021 969 CAACAAGAAMACTTTGAGGAGRGCAAGTGCCTCGAGTCTTGTCGTGGCATCTCCAAGAA 910 601 850 661 790 721 730 781 670 841 610 901 609 AGAGGCCTGGGCTGGGAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTCT 550 549 TGCCTCAGAGACCAGGGCTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCTG 490 430 GGACCTGCCTGCATAGGAGTTTGGAAGTTGGAGTTTTGTTTTCCTCTGTTCAAAGCTG 370 902 TGCCTCAGAGACCAGGGCTCCAGCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTG 961 /LISSUE type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="let strand cDNA was primed with a Not!-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized." Pull-length cDNA libraries and normalization
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Small: seqrefégenoscope.cns.fr, www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODIO7SCGOTNPIkcluster=7854.f. Contact:
Feng Liang Email : fliang@lifetech.com URL:
Location/Qualifiers 482 CAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCCAAGAA 909 GGATGTGTTTGSCKTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGTTGC TGTCGCAGTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATCTTGGGTTACTGCTT 789 CITCAAGAACCAGAGAAAGGACITCCACGGACACCACCACCACCACCACCACCCAGC CAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCACACCACG 669 eccentradecerdesreneacedescreneacedescerdenrecraenracedadec 942 AGAGGCCTGGGCTAGAAAAAACTTTGGAACCCAGACTCTTGCCTGTTTCCCAGGCCCCACTG GGATGTGTTTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACACAGGCTCTGTGGAGATGGC 849 TGTCGCAGTGTTCYTGGTCATCTGCATTGTGGTGGTGGTAGCCATCTTGGGTWACTGCTT CAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCACACGCG GCCCCTCTGAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCTGCCTTGCCAAGGC AGAAAGCTCAAAGGTTTGGAAGGAGCAGAAACCCTTGGGCCAGAAGTACAAATTAGAT 489 AGAAAGCTCAAAGGTTTGGAAGGAGCAGAAACCCTTGGGCCAGAGTACCAGACTAGAT Gaps .. H 60.6%; Score 912; DB 13; Length 1201; larity 97.1%; Pred. No. 2.9e-144; Conservative 5; Mismatches 22; Indels 1. /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DI075YN13" Similarity Best Local Simi Matches 932; 602 Query Match 542 662 722 729 782 962 Bource TITLE JOURNAL COMMENT FEATURES ORIGIN ð 엄 d õ È 셤 ठ 윱 셤 δ ద ò 셤 ò 셤 ò ŝ g à

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I (Dases 1 to 1200)
S. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: sequefogenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1030AC12NP1&cluster=7854.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
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/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lgt strand cDNA was primed with a NotI-oligo(dT)
/primer: Pive prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EORN V sites of the pCMVSPORT 6 vector. Library was normalized."
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Contact: Genoscope
Contact: Genoscope
Genoscope - Centra National de Sequencage
Genoscope - Centra Verance
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Introducted by Life Technologies, a division of
Introduction about this of the France
more information about this cluster, see
http://www.genoscope.cns.fr
cgi?seq=CSODI014CF02NPl&cluster=7854.f. Contact :
cgi.bin/cluster.cgi?seq=CSODI014CF02NPl&cluster=7854.f. Contact :
feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitroGen Corporation 1600
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1 (bases I to 1068)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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Email: seqrefegenoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7884.f For
more information about this cluster, see
more information about this cluster, see
for invitrogen. This sequence if/
cgi-bin/cluster.cgi?seq=CSODIO57BAONP16cluster=7854.f. Contact :
Feng Liang Email: filang@lifetech.com URL
Feng Email: filang@lifetech.com (Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO57BAO3NP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="NHOMO Bapiens"
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/clone lib="strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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1 (bases 1 to 1138)
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1. Inl.-length, cDNA libraries and normalization
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CTGGTACTACAACCCCTTCAGCGAACACTGCGCCCGGCTTTACCTATGGTGGTTGTTACGG Query Match
Best Local Similarity 90.2%;
Matches 980; Conservative Homo sapiens (human) Homo sapiens EST 61 299 121 359 181 419 241 1378 191 1318 ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 13 BX336602 FEATURES ORIGIN 유 셤 δ ò Š 8 δ ద કે 셤 1077 1137 GCCCCAACCCTGTCCTCCGAGCTCCTTTCCATGCTGTGCGCCCCAGGGCTTGGAAG 1197 CCTGAGAAAGCTCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACT 1017 ACTGTGCCTCAGAGACCAGGGCTCCAGCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGT 957 ACTGTGCCTCAGAGACTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCAGGT 492 658 732 777 837 CCCGGCCCTCTGAGCCTGGGCTCACCGGCTCTCACTGGCCCTGCTTCCTGCTTGCCA 612 AGGCAGAGGCCTGGGAAAAATTTGGAACGAGACTCTTGCCTGTTTCCCAGGCC 897 AACAAGAACAACTTTGAGGAAGAGCAGCAGTGCC-TCGAGTCTTGTCGCGGCATCTCCAA 538 910 GAAGGATGTGTTTGGCCTGAGGCGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGAT 598 /organism="Homo sapiens"
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primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized. GCTGCCTGTCCCTACCCCATGGTGCTAGGAAGAGGAGTGGGGGTGGTCAGACCCTGGAG GCCCCAACCCTGTCCTCCCGAGCTCCTCTTCCATGCTGTGCGCCCAGGGCTGGGAAG AGATGGACCTGCCTGCATAGGAGTTTGGAGGTTTGGAGTTTTGTTTTCCTCTGTTCAAA 1258 TGGGTGAAGAGGAAGGGCCTGTTTGGCCTCTCTATCCTCTTCTTCCTCTTCCCCC TG-CCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCACAA GECTETCGCAGTGTTCCTGGTCATCTGCATTGTGGTGGTAGCCATCTTGGGTTACTG GGTACTACAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTG-TTACGGC .. 60 Length 1068; / Match S9.7%; Score 898.4; DB 13; Length Local Similarity 97.0%; Pred. No. 6e-142; nes 987; Conservative 11; Mismatches 12; Indels 838 1078 1198 868 551 928 491 1018 431 371 1138 311 778 719 480 696 539 909 599 850 629 791 731 671 Query Match 셤 品 名 品 谷 र्घ कि र्घ ብ & 台 ઠ 8 8 ð g ઠે g g 음 ద 8 ò 셤 ठे े ઠે

Contact: Genoscope
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Genoscope - Centre National de Sequencage
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Genoscope - Centre National
Bp 191 91006 KVX cedex - France
Bp 191 91006 KVX cedex - Grance
Initiary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSOD1030AC12QP1kcluster=7854.f. Contact :
Feng Liang Email : fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1030AC12QP1. 1377 o mRNA linear EST 02-MAY-2003 COT 25-NORMALIZED Homo sapiens CDNA 'n 418 240 298 120 358 180 Bukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (hases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization (Dnpublished (2001) 72 /organism="Homo sapiens"
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sprimer: Five prime end enriched, double-strand cDNA was
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CAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCAA 538
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BR 191 91006 EVRY cedex - France
division of Invitrogen. This sequence belongs to sequence cluster
7854. For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODH004CA07NP1&cluster=7854.f. Contact:
Feng Liang Brail: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODH004CA07NP1. /tissue_type="T CELLS (JURKAT CELL LINE)"

(Acal line="JURKAT CELL LINE"

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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed

with a NotI-oilgo(dT) primer. Five prime end enriched,

double-errand GDNA was digested with Not I and cloned into

the Not I and EcoRV sites of the pCMVSPORT 6 vector. 'n 478 538 1029 CSSGTKGTACWAAACCCCTYMRSGAACACKCCCCCGCTTTMCTTATGGTG--TTGTTATG 972 912 658 793 718 838 733 778 673 613 898 553 899 CIGIGCCTCAGAGACCAGGGCTCCAGGCCCCTCTTGGAGAAGTCTCAGGTAAGCTCACGTC 958 CIGIGECTCAGAGACTAGAGGCTCCAGCCCTCTTGGAGAAGTCTCAGCTAAGCTCACRWM 493 479 CAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCTCGAGTCTTGTCGCGGCATCTCCCAA 779 GCGGCCCTCTGAGCCTGGGTCTCACCGGCTCTCACCTGGCCTGCTTCCTGGTTGCCAA 672 CCGCCCTCTGAGCCTGGGTCTCACCTGCTCTCACCTGCTTCCTGCTTCCTGCTTGCCAA 419 CTGGTACTACAACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTGGTTGTTACG GAAGGATGTGTTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGTCTGTGGAGAT 599 GGCTGTCGCAGTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATCTTGGGTTACTG TGCCAGCTCCACTGCTCCCACTACCGAGGACACGCAGCACCTGGTCTATAACCACACCACC GGCAGAGGCCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCA TGCCAGCTCCACTGTCTCCACTACCGAGGACACGAGCACCTGGTCTATAACCACACAC GGCAGAGGCCTGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCA 4; Gaps Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 1201) 11, W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Dmpublished (2001) On Feb 16, 2001 this sequence version replaced gi:12944423. Contact: Genoscope Query Match 59.4%; Score 894.4; DB 9; Length 1201; Best Local Similarity 90.6%; Pred, No. 2.7e-141; Matches 931; Conservative 45; Mismatches 48; Indels 4; Library was not normalized." 1. .1201 /organism="Homo sapiens" /mol_type="mRNA" /db xref="taxon:9606" /clone="CSODHO04YB13" 629 539 732 719 839 612 AUTHORS TITLE JOURNAL COMMENT REPERENCE PEATURES 윱 ઠે g ģ 셤 Š å ò ď 8 뭐 ð 셤 ਨੇ 엄 ð

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Contact: Genoscope Marional de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedax - France Bmail: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr
injbrary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1055ABORNI&cluster=7854.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fullingth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1055ABORNPI.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 AMITCCMIGMRMAAMITGIGGCIGTAARAGIWRWMTTITGITTATITAAIGCIRIRGGAT
                    492 AAARAAAGCTCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCCAGAAGTACCAGACTA
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/clone_lib="Home sapiens PLACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Best Local Similarity 97.2%; Pred. No. 5.7e-140;
Matches 912; Conservative 8; Mismatches 16;
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COMPUTEY: USA
ZIP: 94608-2916
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COMPUTER READABLE PORM:
BUDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: LAPPLICATION DATA:
APPLICATION NOTBER: US/09/935,390A
FILING DATE: 22-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NOTBER: 08/986,671
FILING DATE: 1997-12-11
ATTORNEY/AGRY INFORMATION:
NAMME: Jane E. R. POCTER
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET WUMBER: 33,332
TELLECOMMUNICATION INFORMATION:
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Garcia, Pablo
Milliams, Lewis T.
Kothakota, Srinivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emaryville
STATE: CA
US-10-238-183-9
US-10-238-283-9
US-10-238-283-9
US-10-245-14-9
US-10-245-14-9
US-10-245-139-9
US-10-238-325-9
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patent No. US20020076761A1
GENERAL INFORMATION:
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Sequence 1, Appli
Sequence 41, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 11, Appli
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                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-742-201-1
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GTGCCTCAGAGACCAGGGCTCCAGCCCCT
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Patent No. US20020123091A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-09-742-201-1
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; Pred. No. 0;
0; Mismatches
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                                                                                                 ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ 1D NO: US-09-935-390A-4
                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
(510) 655-3542
                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0%;
Matches 1505; Conservative 0;
     TELEFAX:
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APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Kirchhofer, Daniel K.
APPLICANT: Kirchhofer, Daniel K.
APPLICANT: Kirchhofer, Daniel K.
APPLICANT: Kood, William I.
TITLE OF INVENTION: No. US20020123091Alel Inhibitor of Hepatocyte Growth Factor Actinities of INVENTION: for Use in Modulation of Angiogenesis and Cardiovascularization TITLE OF INVENTION: for Use in Modulation of Angiogenesis and Cardiovascularization CURRENT APPLICATION NUMBER: US/09/742,201
CURRENT PLING DATE: 2000-12-19
PRIOR FILING DATE: 2000-02-11
PRIOR PRIOR APPLICATION NUMBER: PCT/US00/06884
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/253,665
PRIOR APPLICATION NUMBER: US 60/253,665 1440 1020 1080 1140 1200 1260 1260 1320 1380 1500 1020 960 960 1141 CCAACCCTGTCCTCCCCAAGCTCCTCTTCCATGCTGCGCCCCAGGGCTGGAAGAACAACAA GIGAAGAGGGGAAGAGGCTGTTTGGCCTCTGTATCCTCTCTTCCTCTTCCCCCAAG GAAGCTCAGCTGCATTCCGCAGCCCCCCAACCCAACAACATCACAGCCCAGCC CAGAGGCTGGGCAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACT GAGAAAGCTCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGA TGGACCTGCCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTTCCTCTCTTCAAAGCT 841

9 8 8 8 B 8 음 성 음 දි සි ર્જ 名 8 셤 1714 TCAAAGGTTTGGAAGGAGCAGAAACCCTTGGGCCAGAAGTACCAACAACATGGACCTG 1028 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428 1534 ACTGTCTCCACTACCGAGGACACGGACCTGTATAACCACACGGGGCCCCTC 788 995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAC 1054 1114 129 GGCAGCTCTGGGGGCTCAGGCGACTTCCCCCAGGGGCCCCTCCATGGAAAGGCGCCATCCA 188
1115 GGCAGCTCTGGGGCTCAGGCGACTTTCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCA 1174 189 GTGTGCTCTGGGACCTGTCAGCCCACTACCGCTGCAGCAATGGCTGCTGCTCGAC 248 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTACGGCAACAAGAAC 488 GIGITECIGGICALCIGCALTGLGGIGGIGGIGGIACATCTGGGITACTGCTTCTTCAAG 668 1835 TGGGCTGGGGAAAACTTTGGAACCGGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA 1894 1029 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC 1088 548 968 608 728 908 69 TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTCGGGTGTGGCAAGGTGGGCCTTTGAGA 128 368 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAAGGG TOGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCGCA GAGACCAGGGCTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCAAGAAGGATGTG 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAC Gaps ö Length 2482; 10; Indels <u>.</u> م 8 Query Match
97.5%; Score 1468; D
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 549 1655 1715 1895 309 1295 369 1355 429 1415 489 1475 1535 1595 1775 849 696 1955 609 699 729 606 6 6 6 6 8 6 6 6 D C 8 8 8 6 8 8 8 8 a 8 8 8 8 8 d දු පු 셤 셤 ઠે 8 8 õ ਨੇ े

US-10-081-056-41

US-10-081-056-41

Sequence 41, Application US/10081056

Publication No. US20040043327A1

GENERAL INRORATION:

APPLICANT: Beaker, Kevin P.

APPLICANT: Gerritsen, Mary E.

APPLICANT: Gerritsen, Mary E.

APPLICANT: Gerritsen, Mary E.

APPLICANT: Gedard, Audrey

APPLICANT: Gedard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Marabers, Scot A.

APPLICANT: Marabers, Scot A.

APPLICANT: Marabers, Scot A.

APPLICANT: Marabers, Colin K.

APPLICANT: Walliam I.

APPLICANT: William P. E. Mickey

APPLICANT: William, P. Mickey

APPLICANT: William, P. Mickey

APPLICANT: William, P. Mickey

APPLICANT: William, S. Mickey

PRIOR APPLICATION NUMBER: US 60/220,664

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1028 1088 2014 CTACCCCATGGTGCTAGGAAGAGAGTGGGGTGCTGAGACCCTGGAGGCCCCAACCCT 1148 1714 1774 1234 1294 1354 1414 1474 1835 TGGGCTGGGAAAAACTTTGGAACCAGACFCTTGGCCTGTTTCCCAGGCCCACTGTGCCTCA 1894 1114 1174 248 728 806 GAGACCAGGGCTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 968 368 788 188 308 428 488 969 TCAAAGGTTTGGAAGGAGGAGAAACCCTTGGGCCAGAGTACCAGACTAGATGGACCTG TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC 2015 CCTGCAFAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTCTCTCTGTTCAAAGCTGCCTGTCC 849 TGGGCTGGGAAAACTTTGGAACCAGACTTTGCCTGTTTCCCAGGCCCACTGTGCCTGA AGTITICCIFGAGIGIGACCACCCCCAACTGCCCCCGACGCCTCCGACGACGCTGCCTGT AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTTGAGA 1029 1089 8 6 ò

Score 1468; DB 13; Pred. No. 0; 0; Mismatches 10;

Query Match
Best Local Similarity 99.3%;
Matches 1474; Conservative

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Length 2482 Indels S

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; TYPE: DNA
; ORGANISM: Homo Sapien
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Sequence A publication US/10145752

Publication No. US2030064473A1

GENERAL INCOPATION:

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APPLICANT: Flvancff Ellen

APPLICANT: Grimadid, Judrey

APPLICANT: Grimadid, Judrey

APPLICANT: Satch, June

APPLICANT: Satch, June

APPLICANT: Satch, Julian

APPLICANT: Fong, Stemman

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REPRENEUR: Pong, Stemman

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE OF INVENTION NUMBER: 06/063046

FROM REPLICATION NUMBER: 60/06304

FROM REPLICATION NUMBER: 60/08609

FROM RELICATION NUMBER: 60/080609

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    Length 2482;
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    DB 13;
Query Match
97.5%; Score 1468; D
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 9
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Pred. No. 0;
0; Mismatches 10;
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Best Local Similarity 99.3%;
Matches 1474; Conservative (
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TYPE: DNA
CRGANISM: Homo Sapien
US-10-245-859-9
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APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Gurmeldi, J. Christopher
APPLICANT: Gurmeldi, J. Christopher
APPLICANT: Gurmeldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Sheman
APPLICANT: Sheman
APPLICANT: Applicant: Watanbe, Colin
APPLICANT: Fong, Sheman
APPLICANT: Tong, Sheman
APPLICANT: Applicant: NOOG William
APPLICANT: APPLICANTON: ACIDS ENCODING THE SAME
APPLICANT: APPLICANTON NUMBER: US/10/245,859
CURRENT FILING DATE: 2002-09-16
FRIOR PILING DATE: 1997-00-17
FRIOR APPLICATION NUMBER: 60/063046
FRIOR FILING DATE: 1997-11-10
FRIOR PILING DATE: 1997-11-10
FRIOR PLING DATE: 1999-03-17
FRIOR PLING DATE: 1998-03-27
FRIOR APPLICATION NUMBER: 60/06304
FRIOR PLING DATE: 1998-03-27
FRIOR APPLICATION NUMBER: 60/06304
FRIOR PLING DATE: 1998-03-27
FRIOR PLING DATE: 1998-03-27
FRIOR PLING DATE: 1998-06-02
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Publication No. US20030064474A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-10-10
PRIOR PILING DATE: 1997-10-10
PRIOR PILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-24
PRIOR PLING DATE: 1997-10-24
PRIOR PLING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR APPLICATION NUMBER: 60/066511
PRIOR APPLICATION NUMBER: 60/066712
PRIOR PLING DATE: 1997-11-24
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-10-211-858-11
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Sequence 11, Application US/10211858
Publication No. US20030211096A1
GENERAL INPORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Margerer, Scot A.
APPLICANT: Pitti, Robert M.
APPLICANT: Pitti, Robert M.
APPLICANT: Pitti, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Scone, Donna M.
APPLICANT: Scone, Donna M.
APPLICANT: Scone, Donna M.
APPLICANT: Wacanabe, Colin K.
APPLICANT: Wacanabe, C
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TYPE: DNA ORGANISM: Homosapiens
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LENGTH: 2482
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ACTGTCTCCACTACCGAGGACACGGACTGTATAACCACACGCGCCCTC
                                 1895 GAGACCAGGCCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC
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                                                                                                      GAGACCAGGCCTCCAGCCCCTTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC
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US-10-305-654-41

US-10-305-654-41

Sequence 41, Application US/10305654

PUBLICATION OF. US20030224984A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Guney, Austin L.
APPLICANT: Hillan, Kemeth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pani, J.
APPLICANT: Pani, J.
APPLICANT: Stephan, J.P. P.
APPLICANT: Stephan, J.P. P.
APPLICANT: Watanabe, C.K.
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APPLICANT: Williams, P.M.

PEPLICANT: Ye, Weilan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS CURRENT SPLICAL WOMERS: US/10/305,654

CURRENT FILLNG DATE: 2002-11-26
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                                   GAGACCAGGGCCCCTCTTGGAGAAGTCTCAGCTAAAGCTCACGTCCTGAGAAAGC 1954
                                                         TCAAAGGTTTGGAAGGAGCAGAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG
                                                                                                             GTAGTTTGTTGTTTTTTATTTAATGCTGTGGGTGAAGAG
       TGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA
                        GAGACCAGGGCCCCTCTTGGAGAAGTCTCAGGTAAGCTCACGTCCTGAGAAAGC
                                                  TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG
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97.5%; Score 1468; DB 15;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10;
PRIOR FILING DATE: 1997-10-24
PRIOR PLING DATE: 1997-10-24
PRIOR PLING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1998-05-2
PRIOR PLING DATE: 1998-05-2
PRIOR PLING DATE: 1998-05-2
PRIOR PLING DATE: 1998-06-2
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-26
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
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CORGANISM: Homo Sapien
US-10-245-103-9
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LENGTH: 2482
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C71
CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US/10/2914
PRIOR APPLICATION NUMBER: 06/063014
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-10-24
PRIOR PLING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 66/065027
PRIOR APPLICATION NUMBER: 66/065027
PRIOR PLING DATE: 1998-03-22
PRIOR PLING DATE: 1998-03-22
PRIOR PLING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 66/08601
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-24
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Pred. No. 0;
0; Mismatches
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US-10-245-107-9
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Sequence 9, Application US/10245107
Publication No. US20030068779A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Stephani, Jean-Phillippe
APPLICANT: Stephani, Jean-Phillippe
APPLICANT: Stephani, Jean-Phillippe
APPLICANT: Stephani, Jean-Phillippe
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, Sherman
APPLICANT: Panay, Zemin
APPLICANT: Panay, Sherman
APPLICANT: Panay, Sherman
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APPLICANT: GLITERALIA, CHINECORDER
APPLICANT: GLITERALIA, CHINECORDER
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Branbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Panag, Sheman
APPLICANT: Panag, Sheman
APPLICANT: Panag, Sheman
APPLICANT: PANAG, SECRITED AND TRANSMEWERANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: 10/197942
PRIOR PELING DATE: 1997-109-10
PRIOR PELING DATE: 1997-10-10
PRIOR PELING DATE: 1997-11-10
PRIOR PELING DATE: 1997-11-10
PRIOR PELING DATE: 1997-11-10
PRIOR PELING DATE: 1999-60-32
PRIOR PELING DATE: 1999-60-32
PRIOR PELING DATE: 1999-60-18
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  Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo Sapien
US-10-245-143-9
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2255 GAGGGGAAGAGGCCTGTTTGGCCTCTTCTCTCTTCCTCTTCCCCCAAGATTGAGCT 2314
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1535 TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCAGGCTCTGTGGAGATGGCTGTCACA 1594
                                                                                  1835 TGGGCTGGGAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCTCTA 1894
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Length 2482;
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RESULT 10
US-10-245-143-9
Sequence 9, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
HAPLICANT: Pilvaroff, Ellen
APPLICANT: Goddard, Audrey

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APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Satch, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Chood, William
APPLICANTON WIMBER: 105/10/245,771
CURRENT APPLICATION WUMBER: 105/10/245,771
CURRENT APPLICANTON WUMBER: 60/063046
PRIOR FLINKO DATE: 1999-10-24
PRIOR FLINKO DATE: 1999-11-10
PRIOR APPLICANTON WUMBER: 60/06307
PRIOR APPLICANTON WUMBER: 60/09369
PRIOR PLINKO DATE: 1998-03-27
PRIOR PLINKO DATE: 1998-06-28
PRIOR PLINKO DATE: 1998-06-38
PRIOR PLINKO DATE: 1
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Pred. No. 0;
0; Mismatches 10;
RESULT 11
US-10-245-771-9
US-10-245-771-9
Sequence 9, Application US/10245771
Publication No. US20030068781A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Bater, Dan
APPLICANT: Filvaroff, Ellen
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Best Local Similarity 99.3%;
Matches 1474; Conservative (
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US-10-245-771-9
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                             GAGACCAGGGCTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCTTGAGAAAGC
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| Oy 1389 GCTGCATTCCGCAGCCCCCCAAGGTTCTCCAACATCACAGCCCAGCCCACT 1448 | RESULT 12 US-10-245-851-9 Sequence 9, Application US/10245851 Fublication No. US.0030068782A1 GENERAL INFORMATION: APPLICANT: Baker Kevin | | APPLICANT: Stephan, Jean-Phillippe APPLICANT: Watanbe, Colin ; APPLICANT: Wood, William ; APPLICANT: Wood, William | APPLICANT: Fong, Sherman TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P. 8630R1093 | CURRENT APPLICATION NUMBER: US/10/245,851 CURRENT FILING DATE: 2002-09-16 ; PRIOR APPLICATION NUMBER: 10/197942 purch Pitted Date: 2002-07-18 | FRIOR FILING DATE: 10/059114 FRIOR FILING DATE: 1997-09-17 FRIOR FILING DATE: 1997-09-17 FRIOR PTI, THOUSER: 60/063046 FRIOR PTI, THOUSER: 1997-10-24 | | APPLICATION P FILING DATE: APPLICATION P FILING DATE: | APPLICATION PRILING DATE: APPLICATION PRILING DATE: | FRIOR APPLICATION NUMBER: 60/090689 ; PRIOR FILING DATE: 1998-06-25 ; Remaining Frior Application data removed - See File Wrapper or PALM. winners of SEO ID NOS: 116 | ; SEQ ID NO 9 ; LENGTH: 2482 ; TYPE: DNA . ORGANISM: Homo Sanien | 97.5%; Score 1468; DB 15; Length 2482; | Conservative 0; Mismatches 10; Indels 0; Gaps CGAGGAGCAGATCTGCAGAGAGAGAGACAACAACAACAACAACAACAACAACAA | Db 995 cccacdedaccacarcriccaacaacarcricarricarcricacacracracracracracracracracracracracra | 3.0 | OY 129 GGCAGCTCTGGGGCTCAGGGGACTTTCCCCCAGGGCCCTCCATGGAAAGGGGCCCATCCA 188 |
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| 309 GAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGAAAGGG 368 | 429 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC 488 | 1475 AACTTTTGAGGAAGGAGCAGCTGCCTGGAGTCTTGTGGGGGCATCTCCAAAAGGATGTG 1534 549 TTTGGCCTGGGGGAAATCCCCATTCCCGGCACAGGCTCTGTGAGATGGCTGTGCA 608 1535 TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGGACACGTTGTGAGATGGCTGTGCA 608 1535 TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGAGAGATGGCTGTCACA 1594 | 609 GIGITCCIGGICALTGIGGIGGIGGIGGIAGCCAICTIGGGITACTGCTICTICAAG 668 | 669 AACCAGAGAAAAGGACTTCCACGGACACCACCACCACCACCACCACCTGCCAGCTCC 728 | 729 ACTGTCTCCACTACCGAGGACACGGAGCACCTGTTAACCACACACGGGGCCCCTC 788 | 789 TGAGCCTGGGTCTCACCGGCCCTGCTTCCTGCTTGCCAAGGCAGAGGCC 848 | 849 TCGGCTGGGAAAAACTTTCGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA 908 | 909 GAGACCAGGGCTCCAGCCCTCTTGGAGAAGTCTCAGCTAAGCTCAGGTCCTGAGAAAGC 968 | 969 TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAACTAGATGGACCTG 1028 | 1029 CCTGCATAGGAGTTTGGAGGAAGTTTGGTTTCCTCTGTTCAAAGCTGCCTGTCC 1088 | 1089 CTACCCATGGTGCTAGGAAGAGAGTGGGGTGTCAGACCCTGGAGGCCCCAACCCT 1148 | 1149 GTCCTCCCGAGGTCCTCTTCCATGCTGTGCGCCCAGGGGAGGAAGAGACTTCCCTGT 1208 | 1209 GTAGTTICHGCTGTAAAGAGTTGCTTTTGTTTATTTAATGCTGTGGCCATGGAAGAG 1268 | 1269 GAGGGGAAGAGGCCTGTTTGGCCTCTTTTCCTCTTTCCCCCAAGATTGAGCT 1328 | AAGCTCA | 2315 CTCTGCCCTTGATCAGCCCCCCCCCTGGCCTAGACCAGCCAG |

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Sequence 9, Application US/10245883

Sequence 9, Application US/10245883

Publication No. US20030068783A1

SAPELICANT: Baker, Kevin

APPLICANT: Baker, Kevin

APPLICANT: Baker, Kevin

APPLICANT: Gland Addrew

APPLICANT: Sandy Amerin

APPLICANT: With ADDREMS AND TRANSWENEARANS POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSWENEARANS POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ALC. BAKES: US/10/245,883

CURRENT APPLICANTON: ACLE BAKES: US/10/245,883

TITLE OF INVENTION: ACLE BAKES: US/10/245,883

CURRENT APPLICANTON NUMBER: US/10/245,883

FRIOR RILING DATE: 1997-19-16

PRIOR APPLICANTON NUMBER: 60/05304

PRIOR APPLICANTON NUMBER: 60/05304

PRIOR PRIOR APPLICATION NUMBER: 60/05057

PRIOR PRIOR APPLICATION NUMBER: 60/050589

PRIOR FILING DATE: 1998-10-22

PRIOR PRIOR APPLICATION NUMBER: 60/050589

PRIOR FILING DATE: 1998-06-12

PRIOR PLING DATE: 1998-06-13

PRIOR PLING DATE: 1998-06-13
                                                                                                                      CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAC
      Query Match

97.5%; Score 1468; DB 15; Length 2482;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 10; Indels 0;
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PRIOR APPLICATION NUMBER: 60/099803
PRIOR PELING DATE: 1998-0-10
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APPLICANT: Baten, Dan
APPLICANT: Baten, Dan
APPLICANT: Baten, Dan
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Swith, Victoria
APPLICANT: Swith, Victoria
APPLICANT: Stephan, Jean Phillippe
APPLICANT: Matambe, Colin
APPLICANT: Matambe, Colin
APPLICANT: Matambe, Colin
APPLICANT: Abang, Zemin
APPLICANT: Chang, Zemin
APPLICANT: Chang, Zemin
APPLICANT: Chang, Zemin
APPLICANT: Pong, Sherman
APPLICANT: ACIDS BNCODING THE SAME
FILE REFERENCE: P3630R1011
CURRENT APLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 60/063104
PRIOR APPLICATION NUMBER: 60/063104
PRIOR APPLICATION NUMBER: 60/063104
PRIOR APPLICATION NUMBER: 60/063104
PRIOR APPLICATION NUMBER: 60/065017
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PILING DATE: 1997-11-10
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Publication No. US20030073189A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR PELING DATE: 2002-01-15
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Pred. No. 0;
0; Mismatches
DR APPLICATION NUMBER: 09/802706

DR FILING DATE: 2001-03-09

DR FILING DATE: 2001-06-01

DR APPLICATION NUMBER: 09/918585

PRILING DATE: 2001-07-30

DR FILING DATE: 2001-07-30

R PILING DATE: 2001-08-06

DR FILING DATE: 2001-08-06

DR FILING DATE: 2001-08-06

DR APPLICATION NUMBER: 09/924419

DR FILING DATE: 2001-08-06

DR APPLICATION NUMBER: 09/923404

PRILING DATE: 2001-08-13

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ALIGNMENTS

Maximum Match 100% Listing first 45 summaries

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Secreted protein; human; cell proliferation; cytokine activity; tissue growth; cellular differentiation; regeneration; activin; inhibin; chemotactic; haemostatic; thrombolytic; tumour inhibition; anti-inflammatory activity; biomarker; ss. This DNA encodes a human secreted protein. The specification provides secreted protein sequences (AAM63681 to AAW63699) encoded by the nucleic acid sequences shown in AAV43601 to AAV43619. The invention provides a Secreted human polypeptides - having cytokine, cell proliferation differentiation, activin or inhibin, tumour inhibition or anti-inflammatory activities. Kothakota /*tag= a /product= "human secreted protein" Garcia P, Williams LT, Human secreted protein 4 encoding DNA. Location/Qualifiers 171. .791 Claim 6; Page 31-32; 78pp; English. 멾 AAV43604 standard; DNA; 1505 97WO-US022787 96US-0032757P 24-SEP-1998 (first entry) WPI; 1998-348453/30. P-PSDB; AAW63684. (CHIR) CHIRON CORP Sacobedo J, Hu Q, Homo sapiens WO9825959-A2 11-DEC-1997; 11-DEC-1996; 18-JUN-1998. AAV43604; Key RESULT 1 AAV43604 cDNA enco Human PRO cDNA enco Human ang Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description

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Query Match:

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SUMMARIES

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Aav43604 H Aad167025 H Abk40259 G Abh88092 H Abk69965 G Abh88092 H Ada01277 H Ada01149 H Ada0114 H

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AAV43604 AAP30055 AAD16721 ABK40259 ABL88092 ABK69965 ABL955811 ADA01277

method of identifying a secreted polypeptide which is modified by rough microsomes. The secreted proteins can be used in assays to determine biological activities, such as cytokine, cell proliferation, or cellular differentiation activities, tissue growth or regeneration, activin or chambian activity, chemotactic or chemokinetic activity, haemostatic or thrombolytic activity, receptor/ligand activity, tumour inhibition, or anti-inflammatory activity. The proteins can also be used as biomarkers, to identify tissues or cell types which expression. They can be used in protein interaction assays, to identify ligands or binding proteins. Or disease-specific alteration in protein expression. They can be used in protein interaction assays, to identify ligands or binding proteins. Compounds which affect the biological activities of the secreted proteins or their ability to interact with specific ligands can be identified or their ability to the protein can also be used to design diagnostic tests and therapeutic compositions for diseases which may be associated with altered expression of these proteins. Fusion proteins can be used to used to target other protein domains to cellular membrane or they can be secreted extracellularly. 888888888888888888888888

Seguence 1505 BP; 332 A; 450 C; 406 G; 317 T; 0 U; 0 Other;

240 999 ö 420 480 480 540 540 600 600 660 CTTTGAGAGGCAGCTCTGGGGGCACTTTCCCCCAGGCCCCTCCATGGAAAGGC 180 180 240 300 300 360 360 420 ACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGGFCTTCTCGCGGCATCTCCAAGA AGGATGTTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGG CTGTCGCAGTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATCTTGGGTTACTGCT GCATOGACAGTTTCCTGGAGTGTGACGACACCCCCCAACTGCCCCCGACGCCTCCGACGAGG GCATCGACAGTTTCCTGGAGTGTGACGACACCCCCAACTGCCCGGACGCCTCCGACGAGG CTGCCTGTGAAAAAAACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCG ACAAAGGGCACTGCCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGT CIGICGCAGTGTTCCTCGTCATCTGCATTGTGGTGGTGGTAGCCATCTTGCGTTACTGCT 0; Gaps Ouery Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; 361 541 481 601 481 543 601 661 661 61 241 301 301 361 61 121 121 181 181 241 g g ठ g ठे D, ò S A ò g g 8 셤 ò ₿ 쉱 ਨੋ g ઠે 셤 Š g Ö

1260 1380 1140 1200 1320 1020 PROSS6; UNQ223; human; immune diseame; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianemmic; immunosuppressive; entithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic; antiallergic; immunostimulant; protease inhibitor; ss. 1080 900 900 960 960 840 840 1081 GCCTGTCCCTACCCCATGGTGCTAGGAGAGAGTGGGGTGGTGGTGGTCAGACCCTGGAGGCC
1081 GCCTGTCCCTACCCCATGGTGCTAGGAAGAGAGGAGTGGGGTGGTGTCAGACCCTGGAGGCC 1381 GAAGCTCAGCTGCATTCCGCAGCCCCCAACGCTTCTCCAACATCACAGCCCAGCC GECCCETCTGAGCTTGGGTCTCACCGGCTCTCACCTGGCCTGCTTGCCAAGG CAGAGGCTGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACT B AAF30055 standard; cDNA; 2482 Human cDNA encoding PRO256 (first entry) GCCGC 1505 30-APR-2001 1501 (1501 AAF30055; 1201 196 721 781 781 841 901 901 961 721 g 윱 g 셤 셤 8 ò ₹ 셤 셤 õ g ठ 셤 ઠે 용장 셤 à ò 셤 ₹ Š 5 6 5 g Š

Location/Qualifiers 188. .1777

Homo sapiens sig_peptide mat_peptide Key

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WO200105972-A1

25-JAN-2001

15-MAR-2000; 2000WO-US006884.

20-JUL-1999; 99US-0144758P.

(GETH) GENENTECH INC.

Godowski PJ; Pitti RM, Tumas D; , Fong S, Goddard A, Mark MR, Marsters SA, Ashkenazi AJ, Baker KP, Gurney AL, Hillan KJ, M Watanabe CK, Wood WI;

WPI; 2001-103149/11. P-PSDB; AAB20113. New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes.

Claim 21; Fig 11; 127pp; English.

The present sequence is that of cDNA clone DNA35880-1160 (ATCC 209379)
centoding novel human immunomodulator protein PR0256 (UM0223) (see
AMB20113). The clone was isolated from a human placenta cDNA library. The
predicted protein (58 ADa, p. 6.22) shows homology to human bikunin,
indicating protease inhibitor activity. The invention provides
completed protein (58 ADA) p. 6.22) shows homology to human bikunin,
indicating protease inhibitor activity. The invention provides
completed proteins (see AAB10050-6.) encoding movel human PR0 proteins (see
AAB20108-20) including PR0256. Claimed compositions comprising these
completed in a mammal of tissue of a mammal, stimulating or enhancing an immune response in a mammal or increasing the proliferation of rimmune response in a mammal or increasing the proliferation of rimmune response in a mammal or increasing the proliferation of rimmune response in a mammal or increasing the proliferation of rimmune response in a mammal in response to an antigen. Claimed compositions
comprising the PRO polypeptide or its antagonist have the opposite
comprising the PRO polypeptide or its antagonist have the opposite
comprising the proliferations antibody. The disorder is selected from
a T cell disorder, involves administering the PRO polypeptide, an agonist
comprising the inflammatory myopathy, Sylogran's syndrome, systemic
inflopathic inflammatory myopathy, Sylogran's syndrome, systemic
inflopathic inflammatory myopathy, Sylogran's syndrome, systemic
chronic active hepatitis, primary biliary dirrhogis, granulomatous
colitis and Crohn's diseases (such as multiple sclerosis), autoimmune
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Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

Query Match

97.5%; Score 1468; DB 4; Length 2482;

| Best Loc Matches Qy Db | cal Similarity 99.3%; Pred. No. 0; 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0; 9 CACGAGGAGCAGATCACAGAGATTCGTTTATGAGGCTCCTTGGGCAACAAGAACAC |
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| ે ઇ | 69 TACCTICGGGAAGAAGAGGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGCCTTTGAGA 12 |
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| 9 8 | 1235 AGITTUCTIGGAGIGTWACCAACACCCCCAACIGCCCCCAACGACGCCTCCGAAGAAGACTGCCTGT 1294 300 GBBBBBBBBCBAGHGAGACAACAAGAAGAAGAAAAAAAAAA |
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| දි සි | 369 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC 428 |
| | 429 AACCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC 4 |
| | 5 AACCCTTCAGGAACACTGCGCCCGCTTTACCTATGGTGTTGTTATGGCAACAAGAAC 14 |
| ර් | 489 AACTTTGAGGAAGAAGCAGCAGGGCGCGAGCTTGTCGCGCGCG |
| q | 1475 AACTITGAGGAAGAGCAGCAGTGCCTCGAGGCCTTCTCGCGGCATCTCCAAGAAGGATGTG 1534 |
| È | 549 TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGGACAGGGCTCTGTGGAAATGGCTGCAGA 608 |
| đ | 1535 TTTGGCCTGAGGCGGGAAATCCCCAGCACAGGCTCTGTGGAGATGGCTGTGACA 1594 |
| දි දි | 609 GTGTTCCTGGTCATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG 668 [[[[|
| Š | an. |
| qa | 1655 AACCAGAGAAAGGACTTCCAGGGACACCACCCACCACCACCACCACCTGCCAGCTGC 1714 |
| ò | 729 ACTGICTCCACTACCGAGGACACGCAGCACCTGGTCTATAACCACCCCACGCGGCCCCTC 788 |
| ģ | 1715 ACTOTOCCACTACCGAGGACACCTGGTCTATAACCACACCCGGCCCCTC 1774 |
| ර සි | 789 TGAGCCTGGGTCTCACCGCTCTCACCTGCCTTCCTGCTAGCCAAGGCC 848 |
| | TGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA 90 |
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| È | 909 GAGACCAGGGCTCCAGCCCCTCTTGGAGAAGTCTCAGGTAAGCTCACGTCCTGAGAAAGC 968 |
| 윤 | CCAGCCCTCTTGGAGAAGTCT |
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| 셤 | TGGAAGGAGCAGAA |
| 8 | 1029 CCTGCATAGGAGTTTGGAAGTTGGAGTTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC 1088 |

2194 1328 1388 2374 1268 2254 2314 CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC 2074 Human, PRO256 protein, cardiovascular, endothelial, angiogenic disorder, cardiac hypertrophy, trauma, cardiant, age-related macular degeneration, gene therapy, adgiogenesis; protease activity, hepatocyte growth factor, peripheral vacular disease; hepato; renal injury, nephrotropic, tumour, restinosis, tranquillizer, vulnerary; cytostatic, hepatotropic, ss. CTCTGCCCTTGATCAGCCCCACCCTGGCCTAGACCAGCAGACAGCCAGGAGAGGCCCA GTAGTTTGTGCTGTAAAGAGTTGCTTTTTGTTTAATGCTGTGGCATGGGTGAAGAG 2195 GTAGTTTGTGCTGTAAAGAGTTGCTTTTTGTTTAATTGCTGTGGCGTGGGTGAAGAG GAGGGGAAGAGGCCTGTTTGGCCTCTCTTCCTCTCTTCCTCTCTCCCCCAAGATTGAGCT CTACCCCATGGTGCTAGGAAGAGGAGTGGGGGTGTCAGACCCTGGAGGCCCCAACCCT CTACCCCATGGTGCTAGGAAGAGAGTGGGTGTCTCAGACCCTGGAGGCCCCAACCCT 2255 GAGGGGAAGAGCCTGTTTGGCCTCTCTCTCTCTTCCTCTTCCCCCAAGATTGAGCT /*tag= " | /*tag= | /*ta Human hepatocyte growth factor activator inhibitor, PRO256 cDNA. Location/Qualifiers 188. .1777 AAD16721 standard; cDNA; 2482 19-DEC-2000; 2000WO-US034756 (first entry) GENENTECH WO200159100-A2 11-FEB-2000; 15-MAR-2000; 28-NOV-2000; 19-NOV-2001 sig_peptide mat_peptide 16-AUG-2001 2015 2075 2315 1389 2375 1449 2435 1089 1149 1209 1269 AAD16721; GETH > Ношо RESULT 3
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The present invention relates to PRO256 or its agonist/antagonist may be used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, especially a human with cardiac hypertrophy, trauma, a type of tumour or age-related macular degeneration. PRO256 may be administered tumour or age-related macular degeneration. PRO256 may be administered tumour or age-related macular degeneration. PRO256 may be administered concentrated agent, a growth inhibitory agent, or angiogenic agent, a chemotherapeutic agent, a growth inhibitory agent, or a cytotoxic agent. PRO256 may also be used to treat the disorders above, preferably through administration via ex vivo gene therapy. PRO256 or its agonist may be used to inhibit endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor, whereas an antagonist of PRO256 may be used to stimulate endothelial cell growth, angiogenesis or protease activity of a hepatocyte growth factor is protease activity of a hepatocyte growth factor is thibition of the protease activity of a hepatocyte growth factor is contained and secret selected from peripheral vascular disease, hepatic or renal injury or a restinosis disorder. The present sequence is human contained to a rethinosis disorder. The present sequence is human contained to a rethinosis disorder. The present sequence is human contained to a rethinosis disorder. The present sequence is human contained to a restinosis disorder. The present sequence is human contained to a restinosis disorder. The present sequence is human contained to a restinosis disorder. The present sequence is human contained to a restinosis disorder inhibitor, RRO256 cDNA.
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1055 TACCTTCGGGAAGAAGAGGCGTTCTAGCCTGTCGGGGGTGTGCAAGGTGGGCCTTTGAGA
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Pred. No. 0;
0; Mismatches 10; Indels
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                                                                                                                                                                Claim 40; Fig 1; 124pp; English.
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Matches 1474; Conservative
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treating

An isolated polypeptide designated PRO256 useful for cardiovascular, endothelial, or angiogenic disorder.

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Kirchhofer

Gurney AL,

74.62.43

WPI; 2001-541567/60. P-PSDB; AAE09332.

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The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, Kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, gilal, astrooytal, hypothalandic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polymolecide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
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leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss.
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Stone DM;
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Pitti RM, Roy MA,
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99US-0123972P
99WS-0133459P
99WS-0140650P
99US-0140653P
99US-014569B
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Best Local Similarity 99.3
Matches 1474; Conservative
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Wood WI;
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P-PSDB; AAU86133.
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Marsters SA, B
Watanabe CK, 1
                                                                Homo sapiens
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11-MAY-1999;
02-JUN-1999;
22-JUN-1999;
20-JUL-1999;
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05-JAN-2000;
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                   GTGTTCCTGGTCATCTGCATTGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG
                                                                               AACCAGAGAAAGGACTTCCACGGACACCACCACCACCACCACCCCTGCCAGCTCC
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TGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA
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                                        AACTTTGAGGAAGAGCAGCAGTGCTCGGAGTCTTGTTGCCGGGGATCTCCCAAGAAGGATGTG
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                                                                                                                                                                                                                                                                                                                                                                             ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardicovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides thrombophlebitis, lymphangitis, tumour including use as hybridisation probes, and in chromosome and gene mapping, and such an including use as hybridisation probes, and in chromosome and gene mapping, and probes used in the
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                                                                                                                                                                   Ę
                                                                                                                                                                                                                                                                         One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                            Ferrara N, Gerber H, Gerritsen ME, Goddard A, PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni FF, Watanabe CK, Williams PM, Wood WI, Ye W;
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99.3%; Pred. No. 0;
ive 0; Mismatches 10; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 41; 565pp; English
25-MAY-2001, 2001US-00866034.
25-MAY-2001, 2001WO-US017092.
30-MAY-2001, 2001WO-US017443.
30-MAY-2001, 2001WO-US017443.
01-JUN-2001, 2001WO-US017800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.3
Matches 1474; Conservative
                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                     WPI; 2002-090516/12.
P-PSDB; ABB84837.
                                                                                                                                                                                  Stephan JF,
                                                                                                                                              Baker KP,
Godowski P
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This invention relates to the cDNA and protein sequences of novel
secreted and transmembrane polypeptides FRO polypeptides. The invention
also comprises a method for producing the protein of the invention means and antibodies specific for the protein of the
invention. The antibody may be used for detecting the PRO proteins of the
invention and may be used for modify their activity. polynucionides may
be used as hybridisation probes for a cDNA library to isolate the full-
length PRO cDNA or to isolate other CDNAs, to construct hybridisation
probes for mapping the gene which encodes that PRO and for genetic
analysis of individuals with genetic disorders, in assays to identify
other proteins or molecules involved in binding reaction, to generate
transgenic animals or knock-out animals which in turn are useful in the
development and screening of therapeutically useful reagents, for
chromosome identification, and tissue typing. The PRO polypeptides are
checomose identification, and tissue typing. The PRO polypeptides are
clectrophoresis purposes. The sequences may also be used to detect
overexpression on PRO polypeptides in cancerous tumours and for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New PRO polypeptides and polynucleotides encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, ogenetic analysis of individuals with genetic disorders.
                                                                                                                                                                                   PRO; secreted protein; transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Goddard A,
Watanabe CK,
                                                                                                                              CDNA encoding human Pro peptide #5.
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Stephan J, W
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genetic disorder; tumour; cancer
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2000US-023547P
2000US-0261870B
2001US-0261910P
2001US-0261939P
2001US-0262150P
2001US-0264395P
2001US-0264395P
2001US-0264395P
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2001US-0274399P
2001US-028982P
2001US-0282129P
2001US-0282199P
2001US-0282199P
2001MO-US017092
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2001WO-US021066
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                                                                           (first entry)
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Smith V,
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16-JAN-2001
16-JAN-2001
16-JAN-2001
25-JAN-2001
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25-JAN-2001
25-JAN-2001
26-FBB-2001
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Fong S,
                            ABK69965;
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1355 CACTGCGTGGACCTGCCAGACACAGGACTCTCCCAAGGAGAGCATCCCGCGCTGGTACTAC 1414
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                                                                                                                                                                                                                                                                                                                                                        1115 GGCAGCTCTGGGGCCTCAGGCGACTTTCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1295 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTCCCCCAGTGACAAGGG 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1475 AACTTTGAGGAGAGCAGCGGAGTGCCTCGAGTCTTGTCGCGGCATCTCCAAGAATGTG 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for differentially expressed genes using microarray technology. The present sequence represents a cDNA encoding a human PRO protein of the invention
                                                                                                                                                                                               995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGGCAACAACAAC
                                                                                                                                                                                                                                                                        1055 TACCTTCGGGAAGAAGAGGGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                               1175 GTGCTCTGGCACCTGTCAGCCCACCCAGTCCGCTGCAGCAAGGCTGCTGCATCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC
                                                                                                                                                                              9 CACCAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCCAACAAGAACAAC
                                                                                                                                                                                                                                                  69 TACCTTCGGGAAGAGAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTGAGA
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                                                                                                                                          Gaps
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                                                                                                        Length 2482;
                                                                       Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
                                                                                                        Score 1468; DB 6; Length 2
Pred. No. 0;
0; Mismatches 10; Indels
                                                                                                      vuery match
Best Local Similarity 99.3%;
Matches 1474; Conservative
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Wood WI, Zhang Z;
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Claim 1; Fig 41; 567pp; English.
                                                                                                                                          22-MAR-2001; 2001US-00815744.

05-APR-2001; 2001US-0081586.

10-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866034.

25-MAY-2001; 2001US-00870574.

30-MAY-2001; 2001WO-US017092.

30-MAY-2001; 2001WO-US0174800.

20-JUN-2001; 2001WO-US017800.
       2000WO-US030952.
2000WO-US032673.
2000WO-US032673.
2000WO-US034956.
2001US-00767609.
2001US-0076650.
2001WO-US06666.
2001US-00806889.
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Godowski PJ, Gurney AL, 1
Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                  GERBER H.
GERRITSEN M E.
GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARGTERS S A.
PAN J.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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FERRARA N.
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       08-NOV-2000;
10-NOV-2000;
20-DEC-2000;
20-DEC-2000;
22-DAN-2001;
28-FEB-2001;
28-FEB-2001;
01-MAR-2001;
01-MAR-2001;
14-MAR-2001;
22-MAR-2001;
25-APR-2001;
10-APR-2001;
10-APR-2001;
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          TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG 1028
                                                         CCTGCATAGGAGTTTGGAGGAGTTTGGAGTTTTGTTTTCCTCTGTTCAAAGCTGCCTGTCC 1088
                                                                      CCTGCATAGGAGTTTGGAGGAAGTTGGAGGAGTTTTGTTTCCTCTGTTCCAAAGCTGCCTGTCC 2074
                                                                                                                                                                                                                                   GTAGTTTGTGCTGTAAAGAGTTGCTTTTTTTTTTAATGCTGTGGCTTGGGTGAAGAG 2254
                                                                                                                                                                                                                                                                                                              CTCTGCCCTTGATCAGCCCCACCCTGGCCTAGACCAGCAGACAAGCCAGGAGAAGCTCA 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; se
                                                                                                                                                                                                                                                           CTCTGCCCTTGATCAGCCCCACCCTGGCCTAGACCAGGCAGAGCCAGGAGGCTCA
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                              1955 TCAAAGGTTTGGAAGGAGAAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACTGGACTG
                                                                                                         CTACCCCATGGTGCTAGGAAGAGAGTGGGGGGTGGTGTCAGACCCTGGAGGCCCCAACCCT
                                                                                                                         GICCICCCGAGCICCICITCCATGCTGCGCCCAGGGCTGGGAGGAAGGACTTCCCTGT
                                                                                                                                                                       GTAGTTTGTGCTGTAAAGAGTTGCTTTTTTTTTTAATGCTGTGGCATGGAGAG
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25-JUL-2000; 2000US-0220664P.
28-JUL-2000; 2000US-0220664P.
28-JUL-2000; 2000US-0220664P.
02-AUG-2000; 2000US-022695P.
17-AUG-2000; 2000US-022695P.
23-AUG-2000; 2000US-US023522.
24-AUG-2000; 2000US-0230978P.
18-SEP-2000; 2000US-0666610.
18-SEP-2000; 2000US-0666510.
24-OCT-2000; 2000US-026952P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL95581 standard; cDNA; 2482
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          696
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thromopolhebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention
                                     Ä
                                                                                                                                                                                                                                               One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction); endothelial or angiogenic disorders in a mammal.
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Goddard A;
SA, Pan J,
WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
Gerber H, Gerritsen ME, G
J, Hillan KJ, Marsters SA,
JK, Williams PM, Wood WI,
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| Db 2135 GTCCTCCCGGGCTCCTTCTTTTTTTTTTTTTTTTTTTT | | Human PRO polymuclec Human; gene; ss; PRC tumour necrosis fact adrenal; lung; colon microvascular endoth sports-related joint | PF 16-SEP-2002; 2002US-002451U7. XX | Fin Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC; FI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z; FI Fong S; XX XX WPI; 2003-625484/59. DR P-PSDB; ADA01278. | NX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, and PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte PT cells. XX XX SS Claim 2; Fig 9; 307pp; English. XX C The invention relates to isolated human PRO polypeptides (secreted and CC transmembrane polypeptides) and the polymucleotides encoding them. The convention also relates to an antibody which specifically binds to a PRO CC polypeptide, a method for stimulating the release of tumour necrosis |
|-------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1055 TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTTGAGA 1128 | 1355 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGACACCCGCGCTGGTACTAC 1414 429 AACCCCTTCAGCGAACACTGCGCCGCTTTACCTATGGTGGTTGTTACGCCAACAAGAACAGAACAGAACAGAACAACAACAACAA | 549 TTTGGCTGAGGGAAATCCCCATTCCGAGGGCTCTGTGGAATGGCTGTGGCGCATTCCCAGGAGGCTCTGTGGAGATGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGAGGCTGTGGAATGGCTGTCGCAGGCTTCCCAGCAGGCTCTGTGGAGTGGCTGCTGTAGGCTTCTCAGGCTTCTGAGGTTACTCTGAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCAGGTTACTCATCAGGTTACTCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGGTTACTCATCAGCCATCATCAGCCATCATCATCAGCCATCATCATCATCATCAGCCATCATCAGCCATCATCAGCCATCATCATCATCATCATCATCATCATCATCATCATCAT | | 1835 IGGGCIGGGGCTCCAGCCTCTTGGAAGTCTCAGCTAAGCTCAGGCCCTGAGAAAGC 909 GAGACCAGGGCTCCAGCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 1895 GAGACCAGGGCTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 969 TCAAAGGTTTGGAAGGAGAAGCCTTGGGGCCAGAAGTACCAGACTAGATGGACTG | 1 2 1 2 1 1 |

cc factor-alpha (TMF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a marmal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating cantisense RNA and pNA and in gene therapy. The polynucleotides may also attisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are used in the development and screening of therapeutically useful.

The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polynucleotide of the invention. 888888888888888888888

Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

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1174 1414 1474 1534 CCCACGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAACAAC 1054 1114 1234 308 1294 1354 809 1594 1654 368 488 788 188 248 428 548 899 69 TACCTTCGGGAAGAAGAGTGCGCTTTCTAGCCTGTCGGGGTGTGCAAGGTGGGGCCTTTTGAGA GECAGCTCTGGGGGCTCAGGCGACTTTCCCCCAGGCCCCTCCATGGAAAGGCGCCATCCA GEGETICTGGCACCTGTCACCCACCCAGTTCCGCTGCAGCAATGGCTGCATCGAC GABABATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGTGACAAAGGG AACCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGAAC AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGGCTCTCCCAAGAAGGATGTG GIGHTCCTGGTCATCTGCATTGTGGTGGTGGTACCCATCTTGGGTTACTGCTTCTAAG CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAC TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGGCCTTTGAGA GGCAGCTCTGGGGCTCAGGCGACTTTCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCA GIGIGCICTGGCACCTGTCAGCCCACCCAGTTCCGCTGCAGCAATGGCTGCTGCATCGAC GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCCAGCGACAAAGGG CACTGCGTGGACTGCCAGACACAGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTAC CACTGCGTGGACCTGCCAGACACAGGACCATCCCGCGCTGCTACTAC AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC AACTITIGAGGAAGGAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCAAGAAGGATGTG TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCGCA 1535 TTTGGCCTGAGGCGGGAAATCCCCCATTCCCAGGCTCTGTGGAGATGGCTGTCACA GTGTTCCTGGTCATCTGCGTTGTGGTGGTAGCCCATCTTGGGTTACTGCTTCTTCAAG ACTGTCTCCACTACCGAGGACACGAGCACCTGGTCTATAACCACACGCGGCCCCTC ö Query Match 97.5%; Score 1468; DB 8; Length 2482; Best Local Similarity 99.3%; Pred. No. 0; Matches 1474; Conservative 0; Mismatches 10; Indels 0; 1055 1475 1595 σ 1115 1175 1235 1295 1355 1415 1655 995 69 129 189 249 309 369 429 489 549 609 699

1028 2014 1088 2074 1148 2134 1208 1268 1328 2314 2374 2434 1894 1954 2194 806 968 1835 recercecananaerringanceancercreecrerinecendences 1895 GAGACCAGGCCCTCTAGGAGAAGTCTCAGCTAAGCTCAAGGTCTCAGGTCTCAGGAAAGC 1955 TCABARGETTTGGBARGGAGCAGABARCCCTTGGGCCAGAAGTACCAGACTAGGACTAGGACCTG CCTGCATAGGAGTTTGGAGGAAGTTGGATTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC CCIGCATAGGAGTITIGAGGAAGTIGGAGTTTTGTTTCTCTCTGTTCAAAGCTGCCTGTCC CTACCCCATGGTGCTAGGAAGAGGAGTGGGGTGTGTCAGACCCTGGAGGCCCCAACCCT 2135 GICCTCCCCGAGGCCCTCTTCCATGCTGTGCGCCCAGGGCTGGGGAAGAACTTCCCTGT TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG GTAGITIGEGCTGTAAAGAGTIGCTTTTTTTTTTTTTTAATGCTGTGGCATGGGTGAAGAG GAGGGGAAGAGGCCTGTTTGGCCTCTCTTCCTCTTCCCCCCAAGATTGAGCT TGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA CTACCCCATGGTGCTAGGAAGAGAGTGGGGTGTCAGACCCTGGAGGCCCCAACCCT GAGACCAGGGCTCCAGCCCCTTGGAGAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 1715 1029 2015 1089 2075 1149 1269 1329 1449 789 849 909 696 1209 2195 2255 1389 2375 2435 å 呂 g g 셤 8 g 셤 g 셤 셤 ò ä ਨੇ ઠ ਨੇ કે ઠે ò ò 셤 ò ठ ઠે

Human cDNA encoding secreted/transmembrane polypeptide PRO256 BP. ADA43706 standard; cDNA; 2482 (first entry) 20-NOV-2003 ADA43706;

ss; gene; human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.

Ношо варіепв

엄 Š 셤

US2003064474-A1

03-APR-2003,

16-SEP-2002; 2002US-00245859 29-AUG-2001; 2001WO-US027099 18-JUL-2002; 2002US-00197942 (GETH) GENENTECH INC. P-PSDB; ADA43707 Gurney AL, Fong S; Saker KP, Fong

or ii

Grimaldi JC; Wood WI, Zhang

Filvaroff E, Goddard A, Stephan JP, Watanabe CK,

Eaton DL, Smith V,

2003-605867/57.

The invention relates to an isolated secreted/transmembrane (PRO)

Co polypeptide, having at least 80% sequence identity to a sequence selected

from any one of the 57 amino acid sequences given in specification, or to
a sequence encoded by a nucleic acid molecule selected from any one of
the nucleic acids deposited under any of the ATCC accession numbers given
in specification, or a sequence having at least 80% identity to PRO
co sequence encoded by a mucleic acid molecule selected from any one of
the nucleic acids deposited under any of the ATCC accession numbers given
in specification, or a sequence having at least 80% identity to PRO
co with or without its associated signal peptide, an extracellular domain of PRO
co with or without its associated signal peptide. Also included are vectors,
transformed host cells, anit-PRO antibodes, the nucleic acids encoding
CC with or without its associated signal peptide. Also included are vectors,
transformed host cells, anit-PRO antibodes, the nucleic acids encoding
CC with or without its associated signal peptide. Also included are vectors,
CC RCO1075, PRO21207, PRO21313 or PRO3134 polypeptide in the above nuclectide
conditional proble derived from any one of the above nuclectide
conditional acides are useful for stimulating the proliferation of human nicrovascular endothelial cells. PRO polypeptides are useful for
colon, breast, prostate, rectal, widney and liver. PRO231, PRO313, PRO3160,
CC PRO3189, PRO4199, PRO6308, PRO6000, PRO10275, PRO21207, PRO2033 and
colon, breast, prostate, rectal, for inducing endothelial cells are useful for inducing genomic and New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 PRO21383, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy. present sequence encodes a PRO protein. Claim 2; Fig 9; 308pp; English.

Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAAGAAG 1054 1055 TACCTTCGGGAAGAAGAGGCCATTCTAGCCTGTCGGGGTGTGCCAAGGTGGGCCCTTTGAGA 1114 TACCTTOGGGAAGAAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTGAGA 128 GGCAGCTCTGGGGCCTCAGCCGACTTTCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCA 188 GTGTGCTCTGGCACCTGTCAGCCCACCCAGTTCCGCTGCAGCAATGGCTGCTGCATCGAC 248 9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAC Gapa ö Score 1468; DB 8; Length 2482; Pred. No. 0; 0; Mismatches 10; Indels 0; Query Match
Best Local Similarity 99.3%;
Matches 1474; Conservative 69 129 ò g ઠે 셤 ò 음

1774 1328 2014 788 369 CACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGGAGCATCCCGGGGCTGGTACTAC 428 668 848 968 1475 AACTITGAGGAAAAAGGAGCAGGCGTCGAGTCTTGTCGCGGGATCTCCCAAGAAGGATGTG 1415 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGAAC AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGCAACAAGAAC AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCAAGAAGGATGTG 549 TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACACACTCTGTGGAGATGGCTGTCGCA 1535 TTTGGCCTGAGGCGGGAAATCCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCACA ACTGTCTCCACTACCGAGGACACGGACCTGGTCTATAACCACACACGCGGCCCCTC TCAAAGGITTGGAAGGAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG GAGGGGAAGAGGCCTGTTTGGCCTCTCTATCCTCTTCCTCTTCCCCCAAGATTGAGCT GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAAGGG GTGTTCCTGGTCTGCATTGTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAG GAGACCAGGCTCCAGCCCCTCTTGGAGAAGTCTCAGCTAAGCTCACGTCAAGAAAGC TCAAAGGTTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG 2015 CCTGCATAGGAGTTTGGAAGTTGGAGTTTTGTTTCCTCTGTTCAAAGCTGCCGTCCC GIAGITITGIGCIGIAAAGAGITIGCTTTTTATTTTAATGCTGTGGCTGAAGAG 2195 GTAGTTTGTGCTGTAAAGAGTTGCTTTTTTGTTTAATTGCTGTGGCATGGGTGAAGAG TGAGCCTGGGTCTCACCGGCTCTCACCTGCCTTCCTGCCTTGCCAAGGCAGAGGCC GAGACCAGGGCTCCAGCCCTCTTGGAGAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC CCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTTCCTCTGTTCAAAGCTGCCTGTCC CTACCCCATGGTGGAAGAAGAGTGGGGTGGTGTCAGACCCTGGAGGCCCCAACCCT CTACCCCATGGTGCTAGGAAGAGGAGTGGGGGTGTCAGACCCTGGAGGCCCCAACCCT 1175 429 489 609 1895 1955 1029 1089 2075 1149 2135 1209 309 699 729 789 849 909 696 1269 g g 쉱 셤 g 셤 Š ġ ģ 셤 à 8 ઠે 유 ઠે ઠે 셤 ò 셤 ŝ 셤 ઠે 臼 ð 셤 8 셤 Š 셤 ò 쉼

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2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or PRO21383 useful for stimulating the proliferation or differentiation of chondrocyte cells and detecting the presence of a tumor in a mammal.
GAGGGGAAGAGCCTGTTTGGCCTCTCTGTCTTCCTCTTCCTCTTCCCCCAAGATTGAGCT
                                GCTGCATTCCGCAGCCCCCACCCCCAAGGTTCTCCAACATCACAGCCCAGCCCCACT
                                                                    ss; gene; human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Grimaldi JC;
Wood WI, Zhang
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Watanabe CK,
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Stephan JP,
                                                                                                                                                               ADA43474 standard; cDNA; 2482
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29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
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                                                                                                                                                                                                       (first entry)
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Smith V,
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P-PSDB; ADA43475.
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and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 pumpan microvascular endothelial cells. PRO POLIFeration of human microvascular endothelial cells. PRO POLIFeration of human microvascular endothelial cells. PRO PRO PROFECT of the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO231, PRO1560, PRO189, PRO6499, PRO6308, PRO6000, PRO1075, PRO21207, PRO231, PRO189, PRO4499, PRO6308, PRO6000, PRO1075, PRO21207, PRO231, PRO189, PRO6499, PRO6400, PRO10775, PRO21207, PRO231, PRO189, PRO6400, PRO10776, PRO189, PRO189, PRO6400, PRO10776, PRO189, PRO1899, PRO6400, PRO107676, PRO1899, PRO5093 and COMMAN of Commation. PRO or the antibody are useful for isolating genomic and cDNA collegonucleotide probes are useful for isolating genomic and cDNA and DNA, and and as antisense probes. PRO nucleic acid is useful as hybridisation probe, in chromosome and gene mapping, in the generation of an antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence encodes a PRO protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1468; DB 8; Length 2
Pred. No. 0;
0; Mismatches 10; Indels
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The invention relates to an isolated secreted/transmembrane (PRO)

polypeptide, having at least 80% sequence identity to a sequence selected

from any one of the 57 amino acid sequences given in specification, or to
a sequence encoded by a nucleic acid molecule selected from any one of
the nucleic acids deposited under any of the ATCC accession numbers given
in specification, or a sequence having at least 80% identity to PRO
lacking its associated signal peptide. Also included are vectors,
transformed host cells, anti-PRO antibodies, the nucleic acids encoding
PRO, PRO fusion proteins, inducing pachhelial cell tube formation (by
administering PRO281, PRO180, PRO189, PRO4499, PRO6308, PRO6600,
PRO16275, PRO21207, PRO2033 or PRO34274 polypeptide or its agonist) and
an oligonucleotide probe derived from any one of the above nucleotide
sequences. PRO6018 polypeptide is useful for stimulating the
proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080

Claim 2; Fig 9; 307pp; English

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Grimaldi JC; Wood WI, Zhang

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696 1955 1029 2015 1089 2075 1149 2135 1209 2195 1269 2255 1329 2315 1389 2375 1449

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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the projection or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. lung, colon, breast, prostate, rectal, kidney and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybrid;sation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides, such as tumours, for stimulating and inhibiting proliferation of human accordant endothelial cells and for inducing endochelial cell tube for inducing endochelial cells at human PRO polynucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1235 AGTTTCCTGGAGTGTGACGACACCCCCAACTGCCCCCGACGACGACGACGACGACTGT 1294
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                                                                                                                                                                                                                                                                                                                                                                     Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in preparation of a medicament for treating a condition responsive to polypeptide, and as therapeutic agents e.g. vaccines.
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Watanabe CK,
                                                                                                                                                                                                                 Filvaroff E,
Stephan JP,
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                                     27-APR-1999; 99US-0131271P.
29-0CT-1999; 99US-0162506P.
02-DEC-1999; 99US-0162506P.
29-AUG-2001; 2001WO-US028551.
18-UUL-2002; 2002US-00197942.
16-SEP-2002; 2002US-00245851
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Smith V,
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Fong S;
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                                                                                                                  1475 AACTTTGAGGAAGAGCAGCAGTGCCTCGAGTTCTTGTCGCGGCATCTCCAAGAAGGATGTG
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                                          AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC
                                                                                                    AACTITIGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCAAGAAGATGTG
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The invention relates to an isolated secreted/transmembrane (PRO)

Comparing at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the mucleic acid molecule selected from any one of the mucleic acid molecule selected from any one of the mucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide. Also included are vectors, it and proper cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1860, PRO189, PRO4499, PRO6308, PRO6000, and processes. PRO6018 polypeptide is useful for stimulating the sequences. PRO6018 polypeptide is useful for stimulating the proliferation of nucleotides can or differation of chondrocyte cells. PRO21383 polypeptides are useful for stimulating the proliferation of number microvascular endothelial cells. PRO6071, PRO6487 and PRO5006 and PRO21383 polypeptides are useful for stimulating the proliferation of chondrocyte cells. PRO18016 collon, breast, prostate, rectal, kidney and liver. PRO5281, PRO1860, PRO189474 polypeptides are useful for inhibiting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO5281, PRO18050, PRO1807474 polypeptides are useful kidney and liver. PRO5281, PRO18050, PRO1807474 polypeptides are useful kidney and liver. PRO5281, PRO18050, PRO18075, PRO21874 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a sequence.
                                                                                                                                                                                                                                                                                                  ss; gene; human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytostatic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in preparation of a medicament for treating a condition responsive to polypeptide, and as therapeutic agents e.g. vaccines.
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Wood WI, Zhang
                                                                                                                                                                                                                                                             Human cDNA encoding secreted/transmembrane polypeptide PRO256
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Watanabe (
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Stephan JP,
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                                                                                                                                         ADA01033 standard; cDNA; 2482
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20-JUN-2001; 2001WO-US019692.
29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
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                                                                                                                                                                                                                      (first entry)
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Smith V,
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Fong S;
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99WO-US01255.
99US-0144758P.
99US-0146222P.
99US-00380137.
2000WO-US008439.
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02-JUN-1999;
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28-JUL-1999;
25-AUG-1999;
30-MAR-2000;
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medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hibridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence encodes a PRO protein.
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                                                                                                                                                                                                                            DB 8; Length 2482;
                                                                                                                                                                                   Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;
                                                                                                                                                                                                                        Score 1468; DB B; Length 2
Pred. No. 0;
0; Mismatches 10; Indels
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Best Local Similarity 99.3%;
Matches 1474; Conservative 0
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Gurney AL, Baker KP, ις Fong WPI;

Filvaroff B, Stephan JP, 02-JUN-2000; 2000WO-US015264. 29-AUG-2001; 2001WO-US027099. 18-JUL-2002; 2002US-00197942. (GETH) GENENTECH INC Eaton DE, Smith V, 2003-585304/55. P-PSDB; ADA43591

Goddard A. Watanabe CK.

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New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO21383, useful in molecular biology, chromosome and genegenerating antisense RNA and DNA, and in gene therapy.

2; Fig 9; 352pp; English. Claim

The invention relates to an isolated secreted/transmembrane (PRO)

polypeptide, having at least 804 sequence identity to a sequence selected from any one of troa any one of the 57 amino acid sequences given in specification, or too a sequence encoded by a nucleic acid molecule selected from any one of troa any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide. Also included are vectors, than for without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the mucleic acids encoding administering PROSI, PROSISO, PROSISO, PROSIOS, P

Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0 U; 0 Other;

1114 1174 ö 1234 128 188 248 995 CCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGGCAACAACAAC 1055 TACCTTCGGGAAGAAGAGGGCATTCTAGCCTGTCGGGGGTGTGCAAGGTGGGCCTTTGAGA GGCAGCTCTGGGGCTCAGGCGACTTTCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCA CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAACAACAAC 69 TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTGAGA GGCAGCTCTGGGGCTCAGGCGACTTTCCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCA Gaps ; 0 Query Match 97.5%; Score 1468; DB 8; Length 2482; Best Local Similarity 99.3%; Pred. No. 0; Masmatches 1474; Conservative 0; Mismatches 10; Indels 0 129 1115 σ 189 셤 쉽 셤 ઠે ò ò

CACTGOGTGGACCGCCAGACACAGGACTCTGCAAGGAGACCATCCGCGCTGGTACTAC 428 AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGAAC 1474 TTTGGCCTGAGGCGGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGGATGGCTGTCACA 1594 AGTTTCCTGGAGTGTGACGACACCCCCCAACTGCCCCCGGACGCCTCCGAGGCTGCCTGT GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATTCCCCAGTGACAAAAGGG 1595 GIGITCCHGGICALCHGCATHGLGGTGGTGGTGCTATCTTGGGTTACTGCTTCTAGG AACCAGAGAGAAAAGGACTTCCACGGACACCACCACCACCACCACCACCCCTGGCTCC 1775 TGAGCCTGGGTCTCACCGGCTCTCACTGGCCCTGCTTCCTGCTTGCCAGGCAGAGGCC AACTITICAAGAAGAAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCAAGAAGGATGTG 1715 ACTIVICOCACTACCGAGGACACCTGGTCTATAACCACACCACCGCCCCCC GAGACCAGGGCTCCACTTTTTTTTCAGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC 1955 TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGAATTAGATGGACCTG 2075 CTACCCCATGGTGCTAGGAGAGAGAGTGGTGTGTCAGACCCTGGAGGCCCCCAACCCT GTAGTTTGTGCTGTAAAGAGTTGCTTTTTTTTTTTAATGCTGTGGCATGGGTGAAGAG GAGGGGAAGCCTGTTTGGCCTCTCTGTCCTCTCTTCCCCCAAGATGAGCT GAAAAATACACGAGGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAAGGG TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCGCA **ACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCACACCACGCGGCCCCTC** TGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCA GAGACCAGGGCTCCAGCCCCTTTGGAGAAGTCTCAGCTAAGCTCACGTCCTGAGAAAGC TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG CCTGCATAGGGGTTTGGGAGGAAGTTGGGTTTTGTTTCCTCTGTTCAAAGCTGCCTGTCC CTACCCCATGGTGCTAGGAAGAGGAGTGGGTGGTGTCAGACCCTGGAGGCCCCAACCCT 2195 Gracificaccioraaacacriccrittificaritaaricchorccafegeraacac GAGGGGAAGAGGCCTGTTTGGCCTCTCTATCCTCTTCTTCCTCTTCCCCCAAGATTGAGCT 1235 309 1295 1355 1415 489 1475 549 1535 699 1655 729 789 849 1835 606 1895 2255 369 1029 1089 1209 1269 249 429 609 696 1149 유 성 ઠે 셤 ઠે g ઠે 셤 ठ 셤 ò d Š 셤 õ d ò 쉱 ò 셤 ò ద ò 뭐 ઠે g ð g ð 셤 ò 셤 ठ 셤 ઠ 뱕 Grimaldi JC; Wood WI, Zhang Z;

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us-09-935-390a-4.rng

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2374
                                                                                                                                                                                                                                      Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNR-alpha; blood; chondrocyte cell; tumou adrenal; lung; colon, breast; prostate; rectum; cervix; liver; microvascular endothelial cell; endothelial cell; tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan, cartilage; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis; helemoglobin-associated disorder; thalassaemia; immune system cell infiltration; cancer; vulnerary; antianaemic; osteopathic; antirheumatic; antiarthritic.
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15-MAY-2000; 2000WO-US013358.
29-AUG-2001; 2001WO-US07099.
18-JUL-2002; 2002US-00197942.
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generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO Polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cells tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human properties.
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Local Similarity 99.3%;
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The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polyrucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte calls and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polymucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and in gene therapy. The polymucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in

Novel secreted and transmembrane polypeptides, PRO polypeptides useful for stimulating proliferation or differentiation of chondrocyte cells inducing endothelial cell tube formation.

Claim 2; Fig 9; 307pp; English

Filvaroff E, Goddard A, Grimaldi JC; Stephan JP, Watanabe CK, Wood WI, Zhang

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Eaton DL, Smith V,

Gurney AL,

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Baker KP,

2003-625486/59. P-PSDB; ADA06853

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ss; gene; osteopathic; antirheumatic; antiarthritic; gene therapy; cell proliferation stimulator; chondrocyte cell differentiation stimulator; chondrocyte cell differentiation stimulator; secreted and transmembrane protein; PRO; human; PRO1313; PRO20080; PRO21383; human microvascular endothalial cell proliferation; PRO6071; PRO4187; PRO606; PRO240; PRO255; PRO698; PRO1002; PRO4316; tumour; adrenal tumour; lung tumour; certal tumour; certal tumour; certal tumour; certal tumour; certal tumour; aprostate tumour; rectal tumour; certal tumour; c
                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane protein PRO256 cDNA.
                                                           ADA08340 standard; cDNA; 2482 BP
                                                                                                                                                                                                                                                                                                    (first entry)
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Homo sapiens

The invention describes an isolated PRO (secreted and transmembrane)

C polypeptide (I). PRO6018 polypeptide is useful for stimulating the

proliferation or differentiation of chondrocyte cells. PRO20080,

C PRO21333 polypeptide is useful for simulating the proliferation of

the man microrascular endothelial cells. PRO6071, PRO487, or PRO6006

polypeptide is useful for inhibiting the proliferation of human

microrascular endothelial cells. PRO polypeptides such as PRO240,

PRO599, PRO1002, PRO4116, etc., are useful for detecting the presence of

tumour in a mammal wich involves comparing the level of expression of

the above mentioned polypeptides in a test sample of cells taken from the

mammal, and a control sample of normal cells of the same cell type, where

the mammal, the tumour being adveral tumour, input tumour, colon tumour in

breast tumour, prostate tumour, rectal tumour, colon tumour in

the mammal, the tumour being adveral tumour, input tumour, colon tumour,

breast tumour, prostate tumour, rectal tumour, or revical tumour,

breast tumour, prostate tumour, rectal tumour, colon tumour,

c compared to the control sample is indicative of the presence of tumour

the mammal, the tumour being adveral tor treating sports-related joint

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c problems, articular cartiage defects, osteoarthritis, or neumour or laver

tumour. PRO6018 polypeptide are useful for screening compounds to

c atthritis. PRO polypeptide are useful for screening compounds to

c ffect of the PRO polypeptide (antagonists) or prevent the

effect of the PRO polypeptide (antagonists). The polymulceotide (II)

and in the generation of anti-ense RNA and DNA.

c ffect of the PRO polypeptide (antagonists) or construct of PRO6018 polypeptides

c floagent native sequence of PRO general publication probes for mapping the general enther transgenic on antivitor profiles in the development and screening of the mapping profiles are also be use Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for stimulating proliferation of human microvascular endothelial cells, and PRO6018 polypeptide useful for stimulating proliferation of chondrocyte Grimaldi JC; Wood WI, Zhang Goddard A, Watanabe CK, m. Filvaroff E, Stephan JP, Claim 2; Fig 9; 308pp; English. 09-MAY-2001; 2001US-0290589P. 29-AUG-2001; 2001WO-US027099. 18-JUL-2002; 2002US-00197942. 16-SEP-2002; 2002US-00245883 (GETH) GENENTECH INC Eaton DL, Smith V, 2003-625488/59. P-PSDB; ADA08341 Baker KP, E Gurney AL, Fong S; 10-APR-2003

ö DB 8; Length 2482; Sequence 2482 BP; 523 A; 792 C; 709 G; 458 T; 0.U; 0 Other; Score 1468; DB 8; Length 24 Pred. No. 0; 0; Mismatches 10; Indels 97.5%; Query Match
Best Local Similarity 99.3
Matches 1474; Conservative δ

| Qy 429 AACCCCTTCAGCGAACATCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC 488 Search completed: J Db 1415 AACCCCTTCAGCGAACATGCCTTTACCTATGGTGGTTGTTATGGCAACAAGAACATGC 1474 J Oy 489 AACTTGAGGAAGAACAGGTGCCTTGAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT | arch completed: D time : 645 sec | SCHOOLS CHOOLS AND CHECK CANAGE AND CHECK CONTROLLS AND CHECK CHOOLS AND C | B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 |
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| 309 GAAAAATACACGAGTTTGACGAGCTCCAGCGCATCCATTCCCCAGCGACAAAGGG 368 | 2255 1329 2315 1389 | 89 GISTGCTCTGGCACCTGTCGCCCACCCACTGCAGCAATGGCTGCTGCACCGCCCCCGCATGGCCCCCGCACGCA | B 성 유 성 |
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| 199 GGCAGCTCTGGGGGCTCAGGGGCCCTCCATGGAAAGGGCCCATCCA 188 Db 2195 | Oy 1149 GTCC Db 2135 GTCC | 69 TACCTTCGGGAAGAGGGGCCATTCTAGCCTGTCGGGGGTGTGCAAGGTGGGCCTTTGAGA 128 | ඊ යි |

earch completed: April 22, 2004, 05:19:43

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

April 22, 2004, 02:57:27; Search time 6021 Seconds (without alignments) 10833 959 Million cell updates/sec

US-09-935-390A-4 1505 Title: Perfect score:

1 GAATICGGCACGAGGAGCAG......AAAAAAAGTCCTGCGGCCGC 1505 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3470272 segs, 21671516995 residues Searched:

6940544 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

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1: gb ba:*
2: gb htg:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| cription | BD063229 Secreted | 7023 S | 32 \$ | ú | 26 | 334 S | 82 | H 6 | 15 Homo | AR123705 Seguence | | 140 Homo E | N | HOMO : | Seque | Homo | Нопо | AR148260 Sequence | E12898 Human cDNA | | | BT007425 Homo sapi | | Ношо | 69 | Ношо | Mus | - | | | Sequenc | m | | 30 Sequenc | | S) | | ě | - | - | - | AX267040 Sequence | m | AX396029 Sequence | BD241950 Compounds | |
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ALIGNMENTS

PAT 27-AUG-2002

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1 (bases 1 to 1505)
Escobedo, J., Hu.Q., Garcia, P., Williams, L.T. and Xothakota, S. Secreted human proteins
Patent: JP 2001505783-A 4 08-MAY-2001;
CHIRON CORP DNA 1505 bp Secreted human proteins. BD063229 BD063229.1 GI:22608832 JP 2001505783-A/4. unidentified unclassified. BD063229 RESULT 1 BD065229 LOCUS DBFINTION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

ORIGIN

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Compositions and methods for the treatment of immune related diseases
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Genentech, Inc. (US)
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Sequence 11 from Patent W00105972.
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PD 08-MAX-2001

PF 11-DEC-1957 UP 1998526977

PI JAIME ESCOBEDO, QUIANJIN HU, PABLO GARCIA, LEWIS T WILLIAMS PI 66/032757

SRINIVAS KOTTAKOTA,

CO7X16/18

CC Strandedness: Single;

CC Topology: Linear;

FN Key

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| FEATURES Location/Qualifiers source 1. 2482 / organism="Homo sapiens" / mol_type="unassigned DNA" / db_xref="taxon:9606" ORIGIN Query Match 97.54; Score 1468; DB 6; Length 2482; Best Local Similarity 99.34; Pred. No. 0; Matches 1474; Conservative 0; Mismatches 10; Indels 0; Gaps 0; | 995 CCCACGAGAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAACAACAACAACAACAACAACAACAACAACAAC | Qy 129 GGCAGCTCTGGGGGCTCAGGCCACTTTCCCCCAGGGCCCTCCATGGAAAGGCGCCATCCA 188 Db 1115 GGCAGCTCTGGGGCCTCTTTCCCCCCAGGGCCCCTCCATGGAAAGCGCCATCCA 1174 Qy 189 GTGTGCTCTGGCCCTGTCAGCCCACCCAGTCCGCTGCAGCAATGGCTGCTGCATGCA | Qy 249 AGTTTCCTGGAGTGTGACCCCCCAACTGCCCCCAACGCCTCCAACGCCTGCTT 308 Db 1235 AGTTTCCTGGAGGTGACGACCCCCAACTGCCCCGACGCCTCCGACGACGCTGCTTT 1294 Qy 309 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGGGCATCCATTTCCCCAGCGACAAAGGG 368 Db 1295 GAAAAATACACGAGTGGCTTTGACGAGCTCCAGGGATCCATTTCCCCAGTGACAAAGGG 1354 Qy 369 CACTGCTGGAGACACAGGACTCTGCAAGGAGACATCCCTGGTGGTACTAC 428 | 1355 CACTGCGTGGACCTGCCAGACACTGCAAGAGAGACATCCGGCGCTGGTACTAC 1414 | | Qy 729 ACTGTCTCCACTACGAGGACACGGAGCACCTGGTCTATAACCACACCACGGGCCCTC 789 T115 ACTGTCTCCACTACCGAGGACACGGACCTGGTCTATAACCACCCCGGCCCTC 1774 Qy 789 TGAGCTGGGTCTCACCGGCTCTCACCTGGTTCCTGCTTGCCAAGGCAGAGGC 848 Db 1775 TGAGCTGGGTCTCACCGGCTCTCACCTGCTTCCTGCTTGCCAAGGCAGAGGC 1834 Cy 849 TGAGCTGGGAAAACTTTGGAACCAACTTCCTGCTTTGCCAAGGCACCTGTGCTCA 1834 Db 1835 TGGGCTGGGAAAACTTTGGAACCAACTTTGCCTGTTTCCCAGGCCACTGTGCTCA 1894 Qy 909 GAGACCAGGGATCCAGCCCTCTTGAGGAAGTCTCAGGCTAAGGTCATGAAAACCTCAGGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAGTCTCAGGCTAAGGCTCAGAAAACTTTGAGAAAGTCTCAGGCTAAGGTCATGAGAAAGC 968 Qy 909 GAGACCAGGGCTCCAGCCCCTCTTGAGGAAGTCTCAGGCTAAAGGTCTCAGGAAAACTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTGAGAAAACTTTAAAAAAAA |

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Patent: WO 202824-A 41 31-3AN-2002.

Genentech, Inc. (US) ; Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gerritsen, Mary E. (US); Goddard, Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Matanabe, Colin K. (US); Williams, P. Mickey (US); Nood, William
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Godowski,P.J., Gurney,A.L., Hillan,K.J., Mareters,S.A., Pan,J.,
Paoni,N.P., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/mol type="unassigned DNA"
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 GTAGTTTGTGCTGTAAAGAGTTGCTTTTTGTTTAATGCTGTGGCATGGGTGAGAGAGGGTGATGCTTTTTTTAATGCTGTGGCATGGGTGAAGAGAGTGCTTTTTTTAATGCTGTGGGATGGGTGAAGAGGTGCTTTTTTAATGCTGTGGGATGGGTGAAGAG
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| FRATURES Location/Qualifiers 1. 2482 1. 2482 . 2482 . 2482 . 2482 / orgalism="Homo sapiens" / mol type="mRNA" / db_xref="taxon:9606" / cone="DNA35880" 1. 2482 1. 2482 | /db_xref="GI. /translation- PAGDCINSFTA ELQPDRCBDAIDA GIPKAWAGIDLW LPQTQTYTSBDHP CQPTQFRCSNGC DLPDTGLCKESII GLRBIPIPSTG GLRRIPIPSTG STVSTTBDTRHIN | Matches 1474; Conservative 0; Mismatches 10; Indelement 1 | 189 GTGTGCTCTGGCACCTGTGAGCCCACCTGTGGCGGCGCATGGGTGCATGGGTGCTGCATGGGTGGTGGGTG | 1415 AACCCCTTCAGCGAACATGCGCTTTACCTATGGTGGTTGTTATGGCAACAAGAAC 1474 |
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| QY 909 GAGACCAGGGCTCCAGGGGAAAGTCTCAGCTAAGGTCATGGAAAAGC 968 Db 1895 GAGACCAGGGCTCCTTTGGAGAAGTCTCAGCTAAGCTCCTGAGAAAGC 1954 QY 969 TCAAAGGTTTGGAAAACCCTTGGACAGAAGTCCAGACTAGATCGACTGTCTGAAAGCTCTGTTCAAAGGTTTGGAAAAACCCTTGGCCAGAAGTACCAGACTAGATCGAACTTGGAAAAACCCTTGTTCAAAGCTGTCCAAAGCTGTCCTGTTCAAAGGTTTGGAAAAACCCTTGTTCAAAGCTGTCCAAAGCTGCCTGTCC 1028 QY 1029 CCTGCATAGGAGTTTGGAAGATTGGAGTTTTTTTTTTTT | 2075 CTACCCCATGGTGCTAGGAAGAGAGTGGTGTCAGACCCTGGAGGCCCCAACCCT 1149 GTCCTCCCCAGCTCGTTCCATGCTGTGGGGTGGTGGGAGGAGGAAGACCTCCTGT 2135 GTCCTCCCCCAGCTCCTTCCATGCTGTGCCCAGGGCTGGGAGGAAGAACTTCCCTGT 2109 GTAGTTTGTGTGTGTAAAGAGTTGCTTTTTTTTTTATTTA | 1329 CTCTGCCCTTGATCAGCCCCAGCCTAGACCAGCAGAGAAAAAAAA | RESULT 8 AY358969 LOCUS DEFINITION Homo sapiens clone DNA35880 HAI-1 (UNQ223) mRNA, complete cds. DEFINITION AY358969 AY388969. GI:37183055 ACCESSION AY358969. GI:37183055 SCHOOL Sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Klimowski, L., Sanchez, C., Lee, J., Lewis, L., Seshagiri, S., Simmons, L., Singh, J., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Stinson, J., Vaggis, A., Vandler, R., Watand, D., Woods, K., Stinson, J., Vaggis, A., Vandler, R., Watanda, D., Wads, K., | Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P. TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment Genome Ree. 13 (10), 2265-2270 (2003) 12975309 12975309 12975309 12975309 1271MS 1217MS |

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rearrousyan, S., Eliott, J.M., Corpuz, R.T., Lazarus, R.A. and Moran, P. Tissue-expression, protease-specificity and Kunitz domain functions of HAI-1B, a new splice variant of hepatocyte growth factor activator inhibitor-1
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SFVYGGCLGNKNNYLREEGILACRGVQGGPLRGSSGAQATPPQGPSMERRHFVVCSGT
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/gene="HAI1"
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Homo sapiens
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Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2370)
Xirchhofer,D., Peek,M., Li,W., Stamos,J., Eigenbrot,C.,
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Hillman,J.L., Tang,Y.Tom., Lal,P., Co
Patterson,C.
Human protease associated proteins
Patent: US 6171790-A 6 09-JAN-2001;
Location/Qualifiers
| Organism="unknown" | / organism="unknown" | / mol_type="unassigned DNA"
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larity 99.4%; Pred. No. 0;
Conservative 0; Mismatches
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Location/Qualifiers
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/forganism='Homo sapiens'
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E I (basea i to 1870)

E Hillan, J. L., Tang, T.Y., Lal, P., Corley, N.C., Guegler, K.J. and Patterson, C.

Human protease associated proteins

I Patent: JP 2002513572-A 2 14-MAY-2002;

INCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002513572-A/2

PP 28-APR-1999 JP 2006547229

PR 01-MAY-1998 US 09/071709

PR 01-MAY-1998 US 09/071709

PI JENNIFER L HILLMAN, TOM Y TANG, PREETI LAL, NEIL C CORLEY, KARL J PI GUEGLER,

PI CHANDRA PATTERSON
                                                                                                                                                                                                                                TCAAAGGTTTGGAAGGAGCAGAAAACCCTTGGGCCAGAAGTACCAGACTAGATGGACCTG 1028
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                                                                                       1238 TGGGCTGGGAAAAACTTTGGAACCAGACTCTTGCCTGTTTCCCAGGCCCACTGTGCCCA
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Human protease associated proteins.
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JP 2002513572-A/2.
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LPQLTVTSSDHPEDTANVTVTVLSTRQTEDYCLASNKVGRCRGSFPRWTYDFTEQICK
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AVAVFLVICIVVVVALLGYCPPKNQRKDFHGHHHPPPTPASSTVSTTEDTEHLVYNH
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortlum/LiNi at: http://image.llnl.gov Series: IRAL Plate: 2 Row: a Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504328.

Location/Qualifiers
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/note="KU; Region: BPTI/Kunitz family of serine protease
inhibitors"
                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Submission Submitsed (01-MRA-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="CDD:cd00109"
1004. .1117
/note="LDLa; Region: Low-density lipoprotein receptor
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.asystemsbiology.org
contact: amadar@asystemsbiology.org
Anup Madan, Jessica Pahey, Brin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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/mol_type="mRNM"

/db_xref="taxon:9606"

/clone="MGC:1726 IMAGE:2959383"

/tissue type="COlon, adenocarcinoma"

/clone Ilb="NIH MGC 15"

/lab hoet="NHOB-R"

/note="Vector: pOTB7"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 2297)

Strausberg, R.L., Feingold, B.A., Grouse, D.H., Derge, J.G.,

Klausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Mang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecon, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Igdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Malek, J.A., Gunatane, P.H., Richards, S.W.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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BC004140
BOOM sapiens serine protease inhibitor, Kunitz type 1, transcript variant 2, mRNA (cDNA clone MGC:1726 IMAGB:2959383), complete cds.
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I (bases 1 to 2486)

Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.R., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mallek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Luy, X. (Gibbs, R.A.,
Norley, K.C., Hale, S., Garcia, A.M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Shavthenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens serine protease inhibitor, Kunitz type 1, transcript variant 2, mRNA clone MGC:15571 IMAGE:3140292), complete cds. BCO18702
BCO18702.1 GI:17511685
MGC.
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/db xref="CDD:smart00192"
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/note="KU; Region: BPTI/Kunitz family of serine protease
inhibitors"
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Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
BC Cancer Agency, Vancouver, BC, Canada
Info@bogger. Do. Can
Steven Jones, Jennifer Asano, Ian Bosder, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,
Letticla Heisto, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Danne Sanilus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Isai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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GIPKAWAGIDLKVQPQEPLVLKDVENTDWRLLRGDTDVRVERKDPNQVELWGLKEGTY
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FLEODOPPUNDPASDEAACRKYTSGEDELQRIHFPSDKGHFVDLDPTGACKESIPRWY
YNPFSEHCAR FTYGGYCKNRANFEEEQQCLSSCHGF SKKUVFGLRREIP IPSTGSVEM
AVAVFLVICIVVVVALLGYCPFRNQRKOFHGHHHPPPPTPASSTYSTTEDTEHLVVNH
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1319. 1474
/note="KU; Region: BPT1/Kunitz family of serine protease
                                                                                                                                                                       Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian
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/note="KU; Region: BPTI/Kunitz family of serine protease
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/note="iDLa; Region: Low-density lipoprotein receptor
Gomain class A<sup>*</sup>
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/clone lib="NIH MGC 21"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
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dmol_type="mkNx""
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/dlone="MGC:15571 IMAGE:3140292"
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/db_xref="locusID:6692"
/db_xref="MIM:605123"
197. .1738
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                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Homo sapiens mRNA for hepatocyte growth factor activator inhibitor,
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Shimomura,T., Denda,K., Kitamura,A., Kawaguchi,T., Kito,M., Kondo,J., Kagaya,S., Qin,L., Takata,H., Miyazawa,K. and Kitamura,N. Hepatocyte growth factor activator inhibitor, a novel Kunitz-type serine protease inhibitor
J. Biol. Chem. 272 (10), 6370-6376 (1997)
                                                                                                                                                                                        GIAGITIGIGCIGIAAAGAGITICCITITIGITITATITIAATGCTGGCATGGGTGAAGAG 2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Denda,K.

Direct Submission

Submitted (24-DBC-1996) Kimitoshi Denda, Tokyo Institute of
Submitted (24-DBC-1996) Kimitoshi Denda, Tokyo Institute of
Technology, Departent of Life Science; 4259 Nagatsuta, Midori-ku,
Yokohama, Kanagawa 227, Japan (B-mail:kdenda@bio.titech.ac.jp,
Tel:45-924-5702, Fax:45-924-5771)
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/prodouct="hepatocyte growth factor activator inhibitor"
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PAGADCIAS FTAGVPGFVLDTUAS VSNIGATELES PTVTKGNICVRACCTTONICIALLY
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| | 634 ACCACCACCACCACCACCACCACACACACACACACACA | , ex 4, ex 4. | Qy B74 GACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCAGAGCCCCCCTCTTG 933 Db 421 GACTCTTGCCTGTTTCCCAGGCCCACTGTGCTCAGAGACCCAGGCTCCAGCCCTCTTG 480 Qy 934 GAGAAGTCTCAGCTACACTCCTGAGAAAGCTTAGAAGAGAAGAAGAAAA 993 Db 481 GAGAAGTCTCAGCTAACTCTCAGAAAAGCTTAGGAAGAAGAAGAAGAAAAAGTTAGGAAAAGAAAAAAA | Oy 994 CCCTTGGGCCAGAAGTACCAGACTAGATGGACCTGCCTGC | 1114 GTGGGTGTGTCAGACCCCCAACCCTGTCCTCCCGGGCTCCTTCCATGC 1173 | 1294 TCTATCCTCTTCCCCCAAGATTGAGCTCTGGATCAGCCCCACCT 1353 | Db 1021 AAAAAAAAAAAAA 1037 |
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| | 1029 CCTGCATAGGAGTTTGGAAGATTGGAGTTTTGTTTCTTCTTCTAAGCTGGCTG | D5 2015 CTACCCCATGGTGCTAGGAAGAGGGGTGGTCAGACCCTGGAGGCCCCAACCCT 2074 | Qy 1269 GAGGGAAGAGGCCTGTTTGGCCTCTCTCTCTCCCCCAAGATTGAGCT 1328 Db 2195 GAGGGAAGAGGCCTGTTTGCCTCTCTCCTCTTCCCCCAAGATTGAGCT 2254 Qy 1329 CTCTGCCCTTGATCAGCCCACCCCCCCCCCCCCCCCCCC | 1389 2315 1449 2375 | RESULT 15 AX067320 AX067320 LOCUS DEFINITION Sequence 24 from Patent W00078960. ACCESSION AX067320 G1:12544944 KEYWOSDS SOURCE Home sapiens (human) ORGANISM Home sapiens (human) Enkaryota; Metazoa; Chordata; Craniata; Buteleostomi; | Mammalia, Eutheria, Primates, Catarrhini, Hominidae CE Yuqiu,J. and Mitcham,J.L. Compositions and methods for the therapy and diagno cancer AL Patent: WO 0078960-A 24 28-DEC-2000; CORIXA CORPORATION (US) Location/Qualifiers L. 103. I. 103. /organism="Homo gapiens" /mol type="unassigned DNA" /db_xref="taxon:9606" | |

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

April 22, 2004, 08:10:04; Search time 2501 Seconds (without alignments) 2459.660 Million cell updates/sec Run on:

US-09-935-390A-23

Perfect score:

Title:

1167 1 MERRHPVCSGTCQPTQFRCS.....TVSTTEDTBHLVYNHTTRPL 206 BLOSUM62 XGapop 10.0 , XGapext YGapop 10.0 , YGapext FGapop 6.0 , FGapext Delop 6.0 , Delext Scoring table: Sequence:

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55026578 Total number of hits satisfying chosen parameters:

27513289 seqs, 14931090276 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| ption | 222 BO687222 | 24 AL558524 AL5 | 950 BX360990 BX36 | 810 BX385810 B | 520 BMB20520 B | 310 CA488310 | 377 CA488377 | 726 BG291726 602388 | 570 BG697670 602660 | 602 BX336602 BX33 | 925 BE79492 | 34.2 4.20 HX3.694.7 | 773 CF14677 | 952 BX33495 | BQ69045 | BG74657 | ALSSOY47 | B187123 | CA48986 | 5 BE74014 | 5 BC020481 | OF13950 | 1 BQ93053 | DESCONDE DESCONDE DESCONDE DE | CB236863 | BG38682 | D BQ89232 | 7 AY416947 | AY416946 | 3 BM008657 | BM844926 | 116 BG38/115 | 113 CT 11 | 267 BE742267 | 29 AL540329 AL540329 | 636 BG821636 | 712 BU696712 LL2in12 | 825 BG609825 323809 | 036 BQ190036 | 627 RX116 |
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ALIGNMENTS

BQ687222 888 bp mRNA linear EST 15-JUL-2002 AGENCORT 8047221 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6207448 5, mRNA sequence.
BQ687222 G1:21812538 BG87222.1 G1:21812538 BG87222.1 Homo sapiens (human) flow sapiens (homo sapiens flow sapie RESULT 1 BQ687222 LOCUS DBFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

us-09-935-390a-23.rst

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structed by Life Technologies, a division of
s sequence belongs to sequence cluster 7854.f For
n about this cluster, see
copp.cns.fr
copp.cns.fr
copicans.fr
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copicans.fr
1: fliang@lifetech.com URL :
th.invitrogen.com/ InVitroGen Corporation 1600
Genoscope sequence ID : CSODJO06BDD7QPI.
                                                                                                                                                                                                                                                                                                                                  1183 bp mRNA, linear EST 31-MAY-2003 ens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED clone CSODJ006YG14 5-PRIME, mRNA sequence.
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CAGTGTTCCTGGTCTCTGCATTGTGGTGGTAGCCATCTTG 572
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1; Primates; Catarrhini; Hominidae; Homo.
13)
                                                                   AGAACCAGGAGAAAGGACTTCCAGGACACCACCACCACCACCA
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Genter National de Sequencage
Genoscope - Centre National de Sequencage
BP 19106 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, web: www.genoscope.cns.fr
Intirgent This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi-seq-CSDD107BBH05QP1&cluster-7854.f. Contact :
Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI07BBH05QP1.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full.length cDNA libraries and normalization
Unpublished (2001)
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  PheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer
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Contract: Genoscope
Genoscope - Centre National de Sequencage
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BP 191 91006 BYRY: cedex - France
Email: sequencecope.cms.fr./ web : www.genoscope.cms.fr./
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7854.f For
more information about this cluster, see
http://www.genoscope.cms.fr/
cgi-bin/cluster.cgi?seq=cS1A1002Z806QPl&cluster=7854.f. Contact:
Feng: Liang@lifeced.com URL
http://filllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1A1002ZB06QPl.
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1 (bases 1 to 1201)
1 (Jases, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                           /organism="Momo mapiens"
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/tissue type="WrACENTA" COT 25-NORMALIZED"
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched (double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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1 [bases 1 to 635]
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                  161 GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisBroPro 180
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                                      845 GGTTACTGCTTCTTCAAGAACCAGAGAAAGGACTTCCACGACACCACCACCACCA
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Korea Research Institute of Bioscience & Biotechnology
Korea Research Institute of Bioscience & Biotechnology
S2 Exemi-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 7 row: H column: 10
Plate: 7 row: H column: 10
High quality sequence stop: 635.
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/clone="S201665307-7-H10"
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High quality sequence stop: 600.

Location/Qualifiers

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Anganism="Homo sapiens"

/ Anganism="Mono sapiens"

/ Ab xref="taxon:9606"

/ Clone="IMAGE:6720058"

/ Clone="IMAGE:6720058"

/ Lab.host="RMDH108"

/ Lab.host="RMDH108"

/ Lab.host="RMDH108"

/ Lone lib="WAPC."

/ Note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I; Subtracted with brain, liver, lung, kidney and muscle birectionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vinneent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.

Manuscript submitted."
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Eukaryota, Metazoa; Chordata, Catarrhini; Hominidae, Homo.

Eutenalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

I (Dases I to 862)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

In Ompublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Clond ciatribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

ttp://image.llnl.gov
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                              TyrAsnProDheSerGluHisCysAlaArgPheThrTyrGlyClyCysTyrGlyAsnLys
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Bukarayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Marmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 973)

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: Kristi A. Egland, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 598.

High quality sequence stop: 598.
                                                       CA488377 973 bp mRNA linear EST 14-NOV-2002 CA488377 MAGE:6720133 5', MRNA SEQUENCE.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mamala; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 663)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 GTGGAGATGCCTGGTGTTCCTGGTCTATCTGCATTGTGGTGGTGGTGGTGGTCTTG 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/note: forgan: forgan: skin; Vector PCMV-SPORT6; Site_1: NotI:
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Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: NGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov h column: 07

Plate: LLAMIOTO row: h column: 07

High quality sequence stop: 662.
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BE794925
601589675F1 NIH_MSC_7 Homo sapiens cDNA clone IMAGE:3943699 5',
145 ValhlaValPheEeuValileCyslleValValValAlalleLeuGlyTyrCysPhe 164
                                                                                                425 GICGCAGIGITICCIGGICAICTCGCAITGIGGGIAGCCAICIIGGGIIACIGCIIC 484
                                                                                                                                                        165 PhelysasuGlmarglysAspPheHisGlyHisHisHisHisBroProProThrProAla 184
                                                                                                                                                                                 185 SerSerThrValSerThrTluAspThrGluHisLeuValTyrAsnHisThrThrArg 204
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Mammalia, Butheria, Primates, Catarihini, Rominidae, Homo.
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Location/Qualifiers
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NIH-MGC http://mgc.nci.nth.gov/.
NIH-MGC http://mgc.nci.nth.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Conteact: Robert Strausherg, Ph.D.
Email: cgapbs-r@mail.inh.gov
Tissue Procurement: DCTD/DTP
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="CSODIOJOYE23"
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/note="lib-"Homo sapiens PlaceNTA COT 25-NORMALIZED"
/note="lib-strand cDNA was primed with a NotI-oligo(dT)
primer. Fave prime end enriched double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                      BX335602 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CONA
BX336602 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODIO30YE23 5-PRIME, mRNA sequence.
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Generacy entre National de Sequencage
Bp 191 91006 EWRY cedex - France
Bmail: Seqrefégencscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
more information about this cluster, see
Mittp://www.genoscope.cns.fr/
Ggi-bin/Juster.cgi?seq=CSDDI030AC12QPIkcluster=7854.f. Contact :
Feng Liarg Email : filangelifetech.com VRL :
http://fulliangth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI030AC12QPI.
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                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (Cases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA librarles and normalization Uppublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 IleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAlaSerAspGluAla 44
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                                                                                                                                       BX336602.1 GI:30339518
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The FANNIUM CORROSTIUM and the RIKEN Genome EXPLORATION RESEARCH Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
Bashawa, R., Nathara, R., Akhhira, S., Akhmura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Fukunishi, Y., Puruno, M., Haragaki, T., Hari, Y., Itoh, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nathara, T., Kawai, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomazaki, R., Ohno, M., Okzaki, Y., Okido, T., Owa, C., Shibeta, K., Shibata, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshida, K., Yoshida, M., Wuramateu, M. and Hayashizaki, Y. Toya, T., Yoshida, Chomes Group, RIKEN Genomic Stences Center (GSC), RIKEN Yokohama Institute, II-722 Suehiro-cho, Tsuruni-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-reseges:riken.go.jp, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) Please visit our web site (http://genome.gsc.riken.go.jp/) Firensch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="head"
/clone lib="RIKEN full-length enriched mouse cDNA library"
       Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pijiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exploration Research
                                                                                                                                                                                                                                                                                                                      Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium and the RIKEN Genome
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| strain="c57BL/6J"
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| db xref="MGI:190766J"
| db xref="MGI:190766J"
| db xref="mGI:1907690"
| c10ne="5430422N02"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKU17442 HTC 20-SEP-2003 MANA linear HTC 20-SEP-2003 Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430425NO2 product:serine protease inhibitor, Kunitz type 1, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIGGAGATGGCTGTCGCAGTTCTGGATTGTGGTGGTGGTGGTAGCCATCTTG 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyTyrCysPhePheLysAsnGlnArglysAspPheHisGlyHisHisHisFiroPro 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleSerLysLysAspValPheGlyLeuArgArgGlulleProlleProSerThrGlySer 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ProThrProAlaSerSerThrValSerThrThrGluAspThrGluHisLeuValTyrAsn 200
                                                                                                                                                                                                                                                                   TCCGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 379
                                                                                                                                                                                                                                                                                                                                                                    AATGGCTGCTGCATCGAGTTTCCTGGAGTGTGACGACACCCCCAACTGCCCCGACGCC 319
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                          AsnGlyCysCysIleAspSerPheLeuGluCyaAspAspThrProAsnCysProAspAla
                                                                                                                                                                                                                                    SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis
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                                                   MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
     US-09-935-390A-23 (1-206) x BE794925 (1-882)
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Mus musculus (house mouse)
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BX369479

BX369479 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens cDNA clone CSGDJ014YC20 5-PRIME, mRNA sequence.
BX369479.1 GI:30457815
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                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapients"
/mol_type="mRNA"
/mol_type="mRNA"
/clone="CSODJO14YC20"
/cell_type="T_CELLS (JURKAT_CELL LINE) COT 10-NORMALIZED"
/cell_thre="JURKAT"
/clone_lib="Homo sapiens T_CELLS (JURKAT_CELL LINE) COT
10-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note==lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pGMVSPORT 6 vector. Library was normalized.
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           1588 ACAACCCAGCCTCTC 1602
206
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                                                         /codom_start=1
/codom_start=1
/protein_id=naba30697.1"
/db xref="GI:12886551"
/db xref="GI:12886551"
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GEDALSACFLANGLYEQNEYCKTAPKEGFINYLTQBLYRSYRELKTRGPGSRIPKIN
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CLGNKNWYLABEBCGLACKTVQGISPKRHPPVCSGSGHATQFRCSHGCTIDGTLKGDD
TPDCPDGSDEATCEKYTSGFDELQNIHFLSDXGYCAELPDTGFRCSHGCTIDGTLKGDD
TPDCPDGSDEATCEKYTSGFDELQNIHFLSDXGYCAELPDTGFRCSHPRWYNPPSE
RCARRETGGCYGKNKNRFEERQQCLESCRGISKKDVFGLRREGSIPTVGSAEVAIAVFL
VICTIVVUTTLGYCFFKNQRKEFHSPLHHPPPTPASSTVSTTEDTEHLVYNHTTQPL"
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                82. _1605
hore="unnamed protein product; putative
serine protease inhibitor, Kunitz type 1
(MGD|MGI:1338033)"
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Matches:
Conservative:
Mismatches:
Indels:
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  dev_stage="6 days neonate"
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BX334952 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0D1009YC11 3-PRIME, mRNA sequence.
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Catarrhini; Hominidae; Homo.
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vert
Mammalia, Butheria, Primates, Catarrhini, Ho
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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VERSION
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Coordinated Laboratory for Computational Genomics
University of Towa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
7E1: 319 335 9265
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Tim Ratlift
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
The following repetitive elements were found at
The following repetitive elements were found in this cDNA
sequence: 426-483, >\TGG)n#Simple_repeat (matched compliment)
Seq primer: DNX-5.
                                                                                                                                                                                                                                                                                                                                                                               CF146773 647 bp mRNA linear EST 06-AUG-2003
UI-HP-CB0-atd-a-02-0-UI.ri NIH MGC_210 Homo sapiens cDNA clone
IMAGE:30570529 5', mRNA sequence.
                                               CysTyrGlyAsnLysAsnAsnPheGluGluGluGluGluGluGluGluCserCysArgGly 120
                                                                                                 IleSerLysLysAspValPheGlyLeuArgArgGluIleProIleProSerThrGlySer 140
                                                                                                                                                  Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 647)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
/organism="Homo sapiens"
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/mol_type="mkNa"
/clone="IMAGE:30570529"
/tissue_type="KOAP4[7]7F-225 cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
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CF146773
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AUTHORS
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/note="Organ: Prostate; Vector: pT7T3 Pac; Site_1: ECOR I; Site_2: Not 1; The library was constructed according bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agence gel. First strand CDNA synthesis was primed with oligo-dT primer containing a Not 1 site. Double strand CDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into PT7T3 Pac vector. The library tag direction promise sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratlift."
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PheAspGluLeuGlnArg11eHisPheProSerAspLysGlyHisCysValAspLeuPro 72
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                                                                                       152
                          52
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                                                  647
0 173
0 0
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                            Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 9100 EVRY cedex - Grant France
BP 191 9100 EVRY cedex - Fra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1133 GCTGCCTKTGAAAAAAAGGGGGGGTTTGACGSAGTCCAGGGGATCCATTTCCCCAGT 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 LysAspValPheGlyLeuArgArgGlulleProlleProSerThrGlySerValGluMet 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGATGTGTTTGGCCTGAGGGGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATG 834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833 ST-GICGCAGTGTTCCTGGTATCTGCATGTGGTGGTGGTGGTAGCCATCTTGGGTTACTGC 775
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      Full-length cDNA libraries and normalization
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TITLE
JOURNAL
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204 ArgProLeu 206
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Search completed: April 22, 2004, 10:13:59 Job time : 2508 secs

Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 9, Appli Sequence 9, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli

Sequence 4, Sequence 8, Sequence 1,

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APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
Quianjin, Hu
Garcia, Pablo
Williams, Lewis T.
Kothakota, Srimivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
US-10-238-346-9
US-10-238-411-9
US-10-243-124-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADRESSE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09935390A Patent No. US20020076761A1 GENERAL INFORMATION:
   US-09-935-390A-4
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2248.855 Million cell updates/sec
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                                                                                                                           US-09-935-390A-23
1167
1 MERRHPVCSGTCQPTQFRCS.....TVSTTEDTEHLVXNHTTRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA:*

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| cgm2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgm2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgm2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgm2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgm2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgm2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgm2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
                                                                            ; Search time 413 Seconds
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                    - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
                                                                           April 22, 2004, 08:23:19
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Xgapp 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Appl Appl Appl

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922 AIGGAAAGGGCCAICCAGIGIGGCTCIGGCACCTGICAGCCCACCAGITCCGCTGCAGG 981
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711 CCCACCCTGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 770
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                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:

AND METHOD OF FRODULING INSPECTOR.

ADDRESSER: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington
CITY: Washington
COMPUTE: 2100 Pennsylvania Avenue, N.W.

COMPUTE: 18M PC compatible
COMPUTE: 22-Jan-2001
PRICHAIN APPLICATION DATA:
APPLICATION NUMBER: 08/685,558
FILING DATE: CUNCHOMN-
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
TYPE: INCLASC acid
FILING DATE: AUCHOMN-
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
TYPE: INCLASC acid
FURNITH: 1542 base pairs
TYPE: INCLASC acid
                                                                                                                                          Sequence 8, Application US/09765449

Patent No. US20020096337A1

GENERAL INFORMATION:

APPLICANT: SHIMOMURA, Takeshi

KAMAUCHI, Tochiya

KITAMURA, Naomi

MIYAZAWA, Keiji

TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME

AND METHOD OF PRODUCING THE PROTEIN

NUMBER OF SEQUENCES: 18
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Matches:
Conservative:
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SEQUENCE DESCRIPTION: SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ANTI-SENSE: ONA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                              771 CACACCACGCGGCCCCTC 788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 108/09/935,390A
FILLING DATE: 22-Aug-2001
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: 08/98,671
FILLING DATE: 1997-12-11
ATTORNAT/AGANT INFORMATION:
NAME: Jan R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION 1065-3542
TELECOMONICATION 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYRE: nucleic acid
STRANDENSS: single
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Matches:
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                                             SerNspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArgIleHis
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APPLICANT: Gerifien, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, Nicholas F.
APPLICANT: Pan, Nicholas F.
APPLICANT: Pan, Nicholas F.
APPLICANT: We selban, Panickey
APPLICANT: We well an I.
APPLICANT: Ye, Wellan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING
FILE REFERENCE: P3235FDC1
CURRENT APPLICANTION NUMBER: US 60/219,556
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR APPLICANTON NUMBER: US 60/220,664
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
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APPLICANT: Berrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
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US-10-081-056-41
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Sequence I, Application US/09742201

Sequence I, Application US/09742201

Setent No. US20020133091A1

GENERAL INFORMATION:

APPLICANT: Gurney, Austin L.

APPLICANT: Wood, William I.

ITILE OF INVENTION: No. US2020133091Alel Inhibitor of Hepatocyte Growth Factor Activ ITILE OF INVENTION: For USe in Modulation of Angiogenesis and Cardiovascularization ITILE OF INVENTION: For USe in Modulation of Angiogenesis and Cardiovascularization ITILE OF INVENTION: P1000/012-19

PRIOR PELICATION NUMBER: PCT/US00/03565

PRIOR APPLICATION NUMBER: PCT/US00/06884

PRIOR PELING DATE: 2000-03-15

PRIOR PPLICATION NUMBER: US 60/253,665

PRIOR PELING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 6

IRNGRED OF SEQ ID NOS: 6

IRNGRED OF SEQ ID NOS: 6

IRNGRED OF SEQ ID NOS: 6
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         81 11eProArgTrpTyrTyzAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly
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US-09-742-201-1
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PRIOR APPLICATION MUNERR, PCT/USO0/20110
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION MUNERR, US 60/224, 655
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR PRIOR PRIOR MUNERR, US 60/230, 978
PRIOR PRIOR DATE: 2000-09-18
PRIOR PRIOR DATE: 2000-11-09
PRIOR PRIOR DATE: 2000-13-09
PRIOR PRIOR DATE: 2000-13-09
PRIOR PRIOR DATE: 2000-13-09
PRIOR PRIOR DATE: 2000-13-09
PRIOR PRIOR DATE: 2001-13-09
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1217 AAIGGCIGCTGCAICGACAGTTICCTGGAGTGTGACGACACCCCCAACTGCCCCGACGCC 1276
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         Length:
Matches:
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is Sequence 9, Application US/10245752

sequence 9, Application Wo. US20030064473A1

GENERAL INFORMATION:

APPLICANT: Bater, Kevin
APPLICANT: Baten, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Growin
APPLICANT: Chang, Zemin
APPLICANT: Pong, Sherman
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APPLICANT: FONG, SHERMAN
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEFTIDES AND NUCLEIC
JITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEFTIDES AND NUCLEIC
JITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C78
CURRENT APPLICATION NUMBER: U6/10/245,859
CURRENT PILING DATE: 2002-09-18
PRIOR PLILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090597
PRIOR PLILING DATE: 1998-06-25
PRIOR PRILING DATE: 1998-06-25
PRIOR PLILING DATE: 1998-06-25
PRIOR PRILING DATE: 1998-06-25
PRIOR PRILING DATE: 1998-06-25
PRIOR PRILING DATE: 1998-06-25
PRIOR PRINCH DATE: 1998-06-25
1577 GTGGAGATGGCTGTCACAGTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATCTTG 1636
                                                   GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro
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Matches:
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watambe, Colin
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Publication No. US20030064474A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
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Fong, Sherman
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ORGANISM: Homo Sapien
US-10-245-859-9
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEFIDES AND NUCLEIC
FILE REPERENCA: PS50R.C66
CURRENT APPLICATION NUMBER: U5/10/245,752
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 06/059114
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-0-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1998-10-24
PRIOR FILING DATE: 1998-10-24
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-02
PRIOR PLILING DATE: 1998-06-04
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILOR DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-24
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US-10-245-752-9
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Best Local Similarity:
Query Match:
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Margareter, Scot A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stone, Donna M.
APPLICANT: Stone, Donna M.
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REFERENCE: P2931RCI
CURRENT FILING DATE: 1994-04-01
PRIOR APPLICATION NUMBER: 60/02694
PRIOR PILING DATE: 1996-04-01
PRIOR PILING DATE: 1996-03-23
PRIOR FILING DATE: 1996-03-23
PRIOR FILING DATE: 1996-03-27
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Publication No. US20030211096A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/05352
PRIOR APPLICATION NUMBER: 60/062037
PRIOR PLING DATE: 1997-09-19
PRIOR PLING DATE: 1997-00-10
PRIOR PILING DATE: 1997-10-10
PRIOR PLING DATE: 1997-10-10
PRIOR PLING DATE: 1997-10-24
PRIOR PLING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR APPLICATION NUMBER: 60/063046
PRIOR APPLICATION NUMBER: 60/066511
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PRIOR PRILING DATE: 1997-11-24
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CRGANISM: Homo sapiens
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APPLICANT: Zhang, Zemin
APPLICANT: Rong, Abernan
APPLICANT: Rong, Abernan
APPLICANTON: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630RIC112
CURRENT APPLICATION NUMBER: US/10/245,103
CURRENT FILING DATE: 100/197942
PRIOR APPLICATION NUMBER: 0/053014
PRIOR PLILING DATE: 1997-0-17
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1998-05-22
PRIOR PLILING DATE: 1998-05-22
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-07
PRIOR PLILING DATE: 1998-06-18
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-25
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                                                                                                                                                     GlyTyrCysPhePheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro
              141 ValGlumetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu
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Matches:
Conservative:
Mismatches:
Indels:
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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Sequence 9, Application US/10245103
Publication No. US20030068778A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
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CRGANISM: Homo Sapien
US-10-245-103-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams, P.M.
APPLICANT: Williams, P.M.
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TRANSMERT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REPERENCE: P3235RLC1
CURRENT APPLICATION NUMBER: US/10/305,654
CURRENT APPLICATION NUMBER: US/10/305,654
CURRENT PILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 41
LENGTH: 2482
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                                                                                  RESULT 8
US-10-305-654-41
Sequence 41, Application US/10305654
Sequence 41, Application US/10305654
GENERAL INFORMATION:
APPLICANT: Beker, Kevin P.
APPLICANT: Perrara, Napoleone; APPLICANT: Gerber, Hand-Peter; APPLICANT: Geritsen, Mary B.
APPLICANT: Geritsen, Mary B.
APPLICANT: Godowski, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
1757 CACACCACCGGCCCCTC 1774
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Paoni, N. F.
Stephan, J-P F.
Watanabe, C.K.
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ORGANISM: Homosapiens
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Best Local Similarity: 9
Query Match:
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Alignment Scores:
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                                                                       1517 ATCTCCAAGAAGAATGTGTTTGGCCTGAGGCGGAAATCCCCATTCCCAGCACAGGCTCT 1576
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Sequence 9, Application US/10245107

Sequence 9, Application US/10245107

Sequence 9, Application US/10245107

Publication No. US20030068779A1

APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Anabe, Colin

APPLICANT: Anabe, Camin

APPLICANT: Anabe, Camin

APPLICANT: Acabe, Semin

APPLICANT: Acabe, Semin

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APPLICANT: Acabe, Sem
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                                           1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
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US-09-935-390A-23 (1-206) x US-10-245-103-9 (1-2482)
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1217 AATGGCTGCTGCGATCGACAGTTTCCTGGAGTGTGACGACACCCCCCAACTGCCCCGACGCC 1276
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FRICK APPLICATION UNDERS: 60/063046
FRICK APPLICATION UNDERS: 60/063046
FRICK APPLICATION UNDERS: 60/065027
FRICK APPLICATION UNDERS: 60/065027
FRICK PILING DATE: 1937-11-024
FRICK PILING DATE: 1936-03-27
FRICK PILING DATE: 1938-05-22
FRICK PILING DATE: 1938-05-22
FRICK PILING DATE: 1938-06-02
FRICK PILING DATE: 1938-06-02
FRICK PILING DATE: 1938-06-018
FRICK PILING DATE: 1938-06-03
FRICK PILING DATE: 1938-06-018
FRICK PILING DATE: 1938-06-03
FRICK PIL
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US-10-245-107-9
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PRIOR APPLICATION NUMBER: 10/197942
PRIOR PILING DATE: 2002-07-18
PRIOR PEPLICATION NUMBER: 60/059114
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1999-10-27
PRIOR PILING DATE: 1999-05-22
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PILING DATE: 1999-05-22
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PRIOR PILING DATE: 1999-06-02
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APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Song, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC
TITLE OF INVENTION: ADDITION ON NUMBER: US/10/245,143
CURRENT PILING DATE: 2002-09-16
PRIOR PLICATION NUMBER: 0/059114
PRIOR PLILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR PLILING DATE: 1997-09-17
PRIOR PLILING DATE: 1998-03-27
PRIOR PLILING DATE: 1998-03-27
PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-25
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-25
PRIOR PLILING DATE: 1998-06-24
PRIOR PLILING DATE: 1998-06-25
PRIOR PRIOR APPLICATION NUMBER: 60/090689
PRIOR PLILING DATE: 1998-06-25
PRIOR PLILING DATE: 1998-06-
1697 CCCACCCCTGCCAGCTCCACTGCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756
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                                                                                                                                   RESULT 11
US-10-245-143-9
Sequence 9, Application US/10245143
Publication No. US20030687B0A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Faton, Dan
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                       Goddard, Audrey
Goddard, Audrey
Grimalio, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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                                                      HisThrArgProLeu 206
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ORGANISM: Homo Sapien
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APPLICANT:
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1637 GGTTACTGCTTCTTCAAGAACCAGAGAAAGAACTTCCACGGACACCACCACCACCACCACCACCA 1696
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1277 TCCGAGGCTGCCTGTGAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 1336
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAMS
FILE REFERENCE: P363 ORACUS
TOTALE OF INVENTION: ACIDS ENCODING THE SAMS
CURRENT APPLICATION NUMBER: US/10/245,771
CURRENT APPLICATION NUMBER: 2002-09-16
                                                                                         1337 TTCCCCAGTGACAAAGGGCACTGCGTGGACCTGCCAGACGACGACGACGACGAGGACTGCAAGAAGGC
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                                                                     Phe ProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSer
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Matches:
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1988-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - 8
NUMBER: OF SEQ ID NOS: 116
SEQ ID NO 9: SEQ ID NOS: 116
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                                                                                                             TYPE: DNA
ORGANISM: Homo Sapien
US-10-245-771-9
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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Sequence 9, Application US/10245851 Publication No. US20030068782A1 GENERAL INFORMATION:

10-245-851-9

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| IlebroArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
                                                             APPLICANT: Grimaldi, J. Christopher
APPLICANT: Senith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Scephan, Jean-Phillippe
APPLICANT: Scephan, Jean-Phillippe
APPLICANT: Scephan, Jean-Phillippe
APPLICANT: Sharman
APPLICANT: Pood, William
APPLICANT: Pood, William
APPLICANT: Pood, William
APPLICANT: Pood, SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE PREFERENCE: PS6.0RLG3
CURRENT FILING DATE: 1002-07-18
PRIOR PLING DATE: 1097-09-17
PRIOR APPLICATION NUMBER: 60/053046
PRIOR PLING DATE: 1997-10-10-10
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1997-11-10
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/09689
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
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Baton, Dan
Filvarceff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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CRGANISM: Homo Sapien
US-10-245-851-9
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1697 CCACCCCTGCCAGCTCCACTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAAC 1756
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; ORGANISM: Homo Sapien
US-10-245-883-9
                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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US-10-237-535-9
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APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
APPLICANT: Tong, Sherman
APPLICANT: Fong, Sherman
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C70
CURRENT PRIJECT 2002-09-16
PRIOR ENTING DATE: 2002-09-16
PRIOR PRICATION NUMBER: 60/055014
PRIOR PLILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1998-06-27
PRIOR PLILING DATE: 1998-06-22
PRIOR PLILING DATE: 1998-06-25
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      1397 ATCCCCCCCTGGTACTACAACCCCTTCAGCGAACACTGCGCCCCCTTTACCTATGGTGGT 1456
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                                                                                                                                                                                                                                                                                           141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu 160
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                                                                                               GlyTyrCysPheDheLysAsnGlnArgLysAspPheHisGlyHisHisHisHisProPro
                                                                CysTyrGlyAsnLysAsnAsnPheGluGluGluGluGlnGlnCysLeuGluSerCysArgGly
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APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Bilen
APPLICANT: Goddard, Audrey
APPLICANT: Gormandi, J. Christopher
APPLICANT: Grimandi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
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LENGTH: 2482
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US-10-245-883-9
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PRIOR APPLICATION NUMBER: 60/206330
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/20932
PRIOR APPLICATION NUMBER: 60/218371
PRIOR PILING DATE: 2000-07-13
PRIOR PILING DATE: 2000-07-13
PRIOR PILING DATE: 2000-09-01
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PRIOR PILING DATE: 2001-01-17
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RAPELICATION NUMBER: 60/199614

RAPLICATION NUMBER: 60/206330

RAPLICATION NUMBER: 60/206330

RILING DATE: 2000-05-23

RAPLICATION NUMBER: 60/206368

RILING DATE: 2000-05-23

RAPLICATION NUMBER: 60/209832

RILING DATE: 2000-06-05

RILING DATE: 2000-06-05

RILING DATE: 2000-06-05

RILING DATE: 2000-07-13

RAPLICATION NUMBER: 60/218371

RAPLICATION NUMBER: 60/218371

RAPLICATION NUMBER: 60/218371
                                                                                                                                                                                   R FILING DATE: 1999-08-20
R APPLICATION NUMBER: 60/151700
R APPLICATION NUMBER: 60/151700
R APPLICATION NUMBER: 60/151734
R FILING DATE: 1999-08-31
R FILING DATE: 1999-08-31
R APPLICATION NUMBER: 60/17026
R FILING DATE: 1999-06-32
R APPLICATION NUMBER: 60/17026
R APPLICATION NUMBER: 60/17026
R APPLICATION NUMBER: 60/17018
R FILING DATE: 2000-01-20
R APPLICATION NUMBER: 60/179851
R FILING DATE: 2000-02-08
R APPLICATION NUMBER: 60/180921
R RILING DATE: 2000-02-08
R FILING DATE: 2000-03-03
                                                                        R FILING DATE: 1999-08-12
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R FILING DATE: 1999-08-17
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R APPLICATION NUMBER: 60/150114
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APPLICATION NUMBER: 60/290589
FILING DATE: 2001-05-09
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ICATION NUMBER: 60/282199
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PRIOR PILING DATE: 2001-04-03
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APPLICATION NUMBER: 60/282129
                                                          APPLICATION NUMBER: 60/148513
    FILING DATE: 1999-08-03
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                  APPLICATION NUMBER:
FILING DATE: 1999-08
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PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
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PRIOR PELING DATE: 1999-03-12
PRIOR PELING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/432131
PRIOR PILING DATE: 1999-10-18
PRIOR PELING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/43297
PRIOR PELING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 2000-10-8
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PRIOR PILING DATE: 2001-09-19
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US-09-935-390A-23 (1-206) x US-10-237-535-9 (1-2482)

1217 AATGGCTGCTGCACACACTTCCTGGAGTGTGACGACACCCCCAACTGCCCCGACGCC 1276 AsnG1 yCysCysIleAspSerPheLeuGluCy8AspAspThrProAsnCy8ProAspAla 40 21 셤 ò g

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81 IleProArgTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100

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1457 TGTTATGGCAACAAGAACAACTTTGAGGAAGAGCAGCAGTGCCTCGAGTCTTGTCGCGGC 1516 161 GlyTyrCysPhePheLygAsnGlnArgLygAspPheHisGlyHisHisHisHisProPro 180 121 IleSerLysLysBapDalPheGlyLeuArgArgGluIleProIleProSerThrGlySer 品 公 品 农 品 农 品 ò 8 8

Search completed: April 22, 2004, 10:22:27 Job time : 422 secs

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Scoring table:

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Searched:

Perfect score:

Run on:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHINGWIRA, Takeshi
APPLICANT: SHAMUGNEA, TOSHIYA
APPLICANT: KAWAGUCHI, TOSHIYA
APPLICANT: KITAMUEA, Naomi
APPLICANT: KITAMUEA, Naomi
APPLICANT: MIYAZAWA, Kabiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER PORM:
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
COMPUTER: BLAN PC Compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,558A
FILING DATE: 24-JUL-1996
FILING DATE: 24-JUL-1995
INPORMATION FOR SEG 1D NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                US-09-439-313-37

US-09-132-149A-37

US-09-152-149A-37

US-09-152-145-37

US-09-115-43-37

US-09-115-43-37

US-09-115-43-37

US-09-115-43-37

US-09-115-43-37

US-09-118-930-63

US-09-128-128-64

US-09-132-149A-15

US-09-15-45-15

US-09-15-48-15

US-09-15-48-15

US-09-118-48-15

US-09-118-48-15

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US-09-118-48-15

US-09-118-48-11

US-09-118-48-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/08685558A ; Patent No. 6225081
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STRANDEDNESS: double
TOPOLOGY: linear
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US-08-685-558A-8
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-WODENE=frame+ p2n.model -DEW=xlh
-WODENE=frame+ p2n.model -DEW=xlh
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-D=/CBT02 1/USPT0 spool/US0993530/runat 2004FIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITSE-Sts -START=1 -BND=-1 -MATRIX=bloeum62 -TRANS=mana140.cdi
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-FGAFEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELIOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (without alignments)
1465.640 Million cell updates/sec
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                                                                                                                                                                                  April 22, 2004, 08:12:09; Search time 78 Seconds
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3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2 6/ptodata/2/ina/6B_COMB.seq:*

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5: /cgn2 6/ptodata/2/ina/PcTUS_COMB.seq:*

6: /cgn2 6/ptodata/2/ina/PctUS_COMB.seq:*
                                 version 5.1.6
- 2004 Compugen Ltd.
                                                                                                                                      protein - nucleic search, using frame_plus_p2n model
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US-09-765-449-8

US-09-071-709-6

US-09-020-956-14

US-09-030-607-14

US-09-352-616A-14

US-09-352-616A-14

US-09-232-149A-14

US-09-232-149A-14

US-09-68-166A-14

US-09-68-166A-14

US-09-68-166A-14

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Copyright (c) 1993
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Matches:
Conservative:
Mismatches:
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                                                                  LOCATION: 1 to 1542
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                                                         NAME/KEY: coding sequence
MOLECULE TYPE: CDNA to mRNA
                                Homo sapiens
                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
          ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: HOMO
                                       STRAIN: MGN45
FEATURE:
                                                                                                                                                                      Alignment Scores:
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US-09-765-449-8
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                                                                                                                                                               Sequence 8, Application US/09765449

Patent No. 6465622

GENERAL INFORMATION:
APPLICANT: RANAGUCHI, Toshiya
KTAMURA, Naomi
MIYAZAWA, Keiji
FITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
AND METHOD OF PRODUCING THE PROTEIN
                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEB: SUCHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
STRAIN: MKN45
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Best Local Similarity:
Query Match:
DB:
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Sequence 14, Application US/09020956

Patent No. 6261562

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 178
COMPRESSPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1039
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STATE: WA
COUNTRY: USA
ZIF: 98104
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                        Conservative:
Mismatches:
Indels:
                                                                                                                                                     US-09-935-390A-23 (1-206) x US-09-071-709-6 (1-1870)
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        121 IleSerLysLysAspValPheGlyLeuArgArgGluIleProlleProSerThrGlySer
                                                                                                                                        141 ValGluMetAlaValAlaValPheLeuValIleCysIleValValValValAlaIleLeu
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Patent No. 617190
GENERAL INVENTION:
APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Gorley, Nail C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
WINNBER OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1870
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COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,709
FILLING DATE: Filed Herewith
CLASSIFICATION:
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3174 PORTER DRIVE
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NAME: CERRONS, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/POCKET NUMBER: PF-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1870 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1522 CACACCACCGGGCCCTC 1539
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLADNOT04
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STATE: CALIFORNIA
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LIBRARY: BLAUNC.
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US-09-071-709-6
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US-09-071-709-6
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81 IleProArgTrpTyrTyzAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGly 100
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| Sequence 14, Application US/09439313 |
| Sequence 14, Application US/09439313 |
| Sequence 14, Application US/09439313 |
| Patent No. 6329656 |
| GENERAL INFORMATION: |
| APPLICANT: Witcham, Jennifer L. |
| APPLICANT: Micham, Jennifer L. |
| APPLICANT: Ralocker, Susan Louise |
| APPLICANT: Ralocker, Susan Louise |
| APPLICANT: Ralos, Michael |
| APPLICANT: Retter, Mark |
| APPLICANT: Retter, Mark |
| APPLICANT: Bay, Craig |
| APPLICANT: OSOL, John |
| APPLICANT: Day, Craig |
| APPLICANT: COMPOSITIONS AND METHODS FOR THERAPY AND |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND |
                OFFRAINS SIEM:

OFFRAINS SIEM:

OFFRAINS SIEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

PLING DATE:

APPLICATION NUMBER:

OCLASSIFICATION:

ATTORNEY/AGENT INPORMATION:

NAME:

REGISTRATION NUMBER:

INFORMATION NUMBER:

TELEFONE:

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TELEFONE:

TELEFONE:

SEQUENCE CLASSIFICATION:

TELEFONE:

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Matches:
Conservative:
Mismatches:
Indels:
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98.20%
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Pred. No.:
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US-09-030-607-14/C

J Sequence 14, Application US/09030607

Sequence 14, Application US/09030607

Patent No. 6262245

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO

NUMBER OF SEQUENCES: 224

NUMBER OF SEQUENCES: 224

NUMBER OF SEQUENCES: 224

NUMBER OF SEGUENCES: 224

NUMBER OF SEGUENC
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STREET: 6:300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
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Matches:
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                                                                                                                                             ATTORNEY FASENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPRENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 682-490
TELEPAX: (206) 682-490
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 base pairs
TERNITH: 816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
    CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFTCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
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ORGANISM: Homo sapien
FEATURE:
; LOCATION: (1)...(816); OTHER INFORMATION: n
US-09-352-616A-14
                                                                                     Percent Similarity: Sest Local Similarity: 9 Query Match: DB:
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Best Local Similarity:
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Pred. No.:
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patent No. 6395270;

patent No. 6395270;

patent No. 6395270;

patent No. 6395270;

APPLICANT: Dillon, Davin C.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: OP PROSTATE CANCER AND DIAGNOSIS

TITLE OF INVENTION: OP PROSTATE CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: OP PROSTATE US/09/352,616A

CURRENT APPLICATION NUMBER: US/09/352,616A

CURRENT FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 472

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 14

LENGTH: 816
                                                                                                                                                                                                                                                                                        816
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                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
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       DIAGNOSIS OF PROSTATE CANCER
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 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE FILE REPRENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 816
                                                                                                                                                                                          ) OTHER INFORMATION: n = A,T,C or G
US-09-439-313-14
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NAME/KEY: misc_feature
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                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
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US-09-352-616A-14/c
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21S TCGGACGAGCCTGCTGTGAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCAT 156
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                                                                                                                                                                                                       21 AsnGlyCysCysIleAspSerPheLeuGluCysAspAspThrProAsnCysProAspAla
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US-09-232-149A-14/C

Sequence 14, Application US/09232149A

Patent No. 6455611

SEGURRAL INFORMATION:
APPLICANT: Wi. Jiangchun

APPLICANT: Mitcham, Jenning.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF CURRENT APPLICATION NUMBER: US/09/232,149A

CURRENT APPLICATION NUMBER: US/09/232,149A

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH.: 816
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                                                                                                             US-09-935-390A-23 (1-206) x US-09-352-616A-14 (1-816)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 CysTyrGlyAsnLysAsnAsnPheGluGluGlu 111
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OTHER INFORMATION: n = A,T,C or
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647.00
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215 TCGGACGAGGCTGCCTGTGAAAAAAAAAGAGGCTTTGACGAGGCTCCAGCGCATCCAT 156
            41 SerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArglleHis 60
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GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Stann L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fetter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Wedvick, Thomas S.
APPLICANT: Medvick, Thomas S.
APPLICANT: Medvick, Thomas S.
APPLICANT: Medpler, Milliam
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hoper, William
APPLICANT: Hoper, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: BERERENCE: 210121.42717C17
CURRENT APPLICATION UNDER: US/09/636,215
CURRENT PILLNG DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
CURRENT PILLNG DATE: 2000-08-10
SEQ ID NO HERENCE FREENCE FREENC
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                                                                                            101 CysTyrGlyAsnLysAsnAsnAbeGluGluGluGlu 111
                                                                                                                    35 TGTTATGGCAACAAGAACAACTTTGAGGAAGAG 3
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; Sequence 14, Application US/09636215
; Patent No. 6520922
; GENERAL INFORMATION:
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NAME/KEY: misc_feature

LOCATION: (11...(816)

OTHER INFORMATION: n = A,T,C
US-09-636-215-14
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ORGANISM: Homo sapien
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US-09-159-114/c
Sequence 14, Application US/09159812A
Sequence 14, Application US/09159812A
Sequence 14, Application US/09159812A
GENERAL INFORMATION:
APPLICANT: Xu, Jaingchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSERVE CANCER AND METHODS FOR THEIR USE
CURRENT PELLOTION NUMBER: US/09/159,812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SEQ ID NO 14
LENGTH: 916
LENGTH: 916
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; NAME/KEY: misc feature
; LOCATION: (1)...(816)
; OTHER INFORMATION: n = A,T,C or US-09-159-812-14
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'US-09-115-453-14/c

'US-09-115-453-14/c

'Sequence 14, Application US/09115453B

'Batent No. 6657056

'GENERAL INPOWNATION:

'APPLICANT: Xu, Jiangchun

'APPLICANT: Dillon, Davin C.

'TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

'TITLE OF INVENTION: METHODS FOR THEIR USE

'PILE REFERENCE: 210121.427C4

'CURRENT APPLICATION NUMBER: US/09/115,453B

'CURRENT PILLING DATE: 1998-07-14

'NUMBER OF SEQ ID NOS: 228

'SOUTHARE: PastSEQ for Windows Version 3.0

'SEQ ID NO 14

LENGTH: 816
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; Sequence 14, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION;
; APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(816)
COTHER INFORMATION: n = A,T,C or G
US-09-115-453-14
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ORGANISM: Homo sapien
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                                                                                                                                              RESULT 11
US-09-685-166A-14/C
| Sequence 14, Application US/09685166A
| Patent No. 663030E
| GENERAL INFORMATION:
| APPLICANT: Xu, Jiangchun
| APPLICANT: Allon, Davin C.
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Harlocker, Susan L.
| APPLICANT: Fanger, Wobert A.
| APPLICANT: Fanger, Mohert A.
| APPLICANT: Fanger, Michael D.
| APPLICANT: Fanger, Mark M.
| APPLICANT: Fanger, Mark M.
| APPLICANT: Stolk, John A.
| APPLICANT: Stolk, Milliam C.
| APPLICANT: Mang, Ailun
| APPLICANT: Hepler, William
| APPLICANT: Hepler, William
| TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
| FILE REFRENCE: 21011.42721
| CURRENT APPLICANT: William
| TITLE OF INVENTION: UNMER: US/09/685,166A
| CURRENT FILING DATE: 2000-10-10
| NUMBERS OF SEQ ID NOS: 898
| SOFTWARE: FastSEQ for Windows Version 3.0
| LEWANTH: Habler, Mindows Version 3.0
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; OTHER INFORMATION: n = A,T,C
US-09-685-166A-14
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: U9-FBE-1998
CLASSIFICATION:
ATTONREY/AGENT INPORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REBERRICE/DOCKET NUMBER: 210121.427C2
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 632-4900
TELEPHONE: (206) 622-4900
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US-09-020-956-37
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Best Local Similarity:
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US-09-030-607-37/c
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Sequence 37, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
CANDIDAN: VI. Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR EXPENSES SEED and BERRY LLP
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 99104
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   APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427D2
CURRENT APPLICATION NUMBER: US/09/688,489
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 816
TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                       FEATURE:
NAME/KBY: misc feature
LOCATION: (1)...(816)
OTHER INFORMATION: n = A,T,C
US-09-688-489-14
                                                                                                                                                                                                                                                                                                                                                               3.55e-62
647.00
99.10%
98.20%
55.44%
                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-020-956-37/c
                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
Score:
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us-09-935-390a-23.rni

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341 ATGGAAAGGCC-NATCCAGTGTGTTCTGGCACCTGTCAGCCCACCCAGTTCCGCTGCAGG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 IIIeProargTrpTyrTyrAsnProPheSerGluHisCysAlaArgPheThrTyrGlyGl 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 aSerAspGluAlaAlaCysGluLysTyrThrSerGlyPheAspGluLeuGlnArglleHi 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 sPheProSerAspLysGlyHisCysValAspLeuProAspThrGlyLeuCysLysGluSe 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetGluArgArgHisProValCysSerGlyThrCysGlnProThrGlnPheArgCysSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 carcececeregraciacaacecerreaceaacacidececerracerations 43
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: Z5-FEB-1998
CLASSIPECATION:
NAME: Mach: David: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
FELEPRAYION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
FELEPAXION NUMBER: 20010
FELEPAX: (206) 622-4900
TELEPAX: (206) 622-6001
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: LENGTH: ADNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yCysTyrGlyAsnLysAsnAsnPheGluGluGluGln 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-935-390A-23 (1-206) x US-09-030-607-37 (1-760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.85e-54
572.00
92.92%
91.15%
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
US-09-030-607-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
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Search completed: April 22, 2004, 10:15:22 Job time : 82 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 22, 2004, 04:43:13; Search time 123 Seconds

(without alignments)

6790.253 Million cell updates/sec
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Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | ý | ωÌ | æ | 7 | 4 | 7,4 | 14 | 14, | 14 | 14, | Sequence 14, Appl | 14, | 14, | 37, | (F) | Sequence 37, Appl | 37, | 37, | 37, | | | Sequence 37, Appl | | 15, | - | 15, | |
|---------------|---------------|------------------|-----------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|
| QI | -09-071-709-6 | US-08-685-558A-8 | US-09-765-449-8 | US-09-020-956-14 | US-09-030-607-14 | US-09-439-313-14 | US-09-352-616A-14 | US-09-232-149A-14 | US-09-159-812-14 | US-09-636-215-14 | US-09-685-166A-14 | US-09-115-453-14 | US-09-688-489-14 | US-09-020-956-37 | US-09-030-607-37 | US-09-439-313-37 | US-09-352-616A-37 | US-09-232-149A-37 | US-09-159-812-37 | US-09-636-215-37 | US-09-685-166A-37 | US-09-115-453-37 | US-09-688-489-37 | US-09-020-956-15 | US-09-030-607-15 | US-09-439-313-15 | US-09-352-616A-15 |
| DB | m | m | 4, | m | m | 41 | 4 | 7 | 4 | 4 | ٦, | 4 | 4 | m | m | ぜ | ゼ | 4 | 4 | 4 | 4 | 4 | 4 | 'n | m | 꺅 | 4 |
| Length | 1870 | 1542 | 1542 | 816 | 816 | 816 | 816 | 816 | 816 | 816 | 816 | 816 | 816 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 760 | 783 | | | 783 |
| Query | 6.96 | 44.3 | 44.3 | 27.5 | 27.5 | 27.5 | 27.5 | 27.5 | 27.5 | 27.5 | 27.5 | 27.5 | 27.5 | 23.8 | 23.8 | 23.8 | 23.8 | 23.8 | 23.8 | | 23.8 | 23.8 | 23.8 | 16 | ٦ | 16 | - |
| Score | 1458.6 | 667.4 | 667.4 | 413.4 | 413.4 | 413.4 | 413.4 | 413.4 | 413.4 | 413.4 | 413.4 | 413.4 | 413.4 | 357.8 | 357.8 | 357.8 | 357.8 | 357.8 | 357.8 | 357.8 | | 357.8 | 357.8 | 246.4 | 4.6 | 45 | 246.4 |
| ult No. | . ~1 | N | m | 4 | Ŋ | 9 | [~ | œ | თ | 0 | H | 12 | 13 | 14 | 12 | 16 | 7 | œ | 5 | 20 | 27 | 22 | 23 | 24 | 52 | 26 | 23 |
| Result No. | ! | | | U | O | υ | O | O | υ | U | U | U | U | U | O | U | υ | υ | υ | U | U | υ | υ | | | | |

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Gaps

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Indels

Query Match 96.9%; Score 1458.6; Best Local Similarity 99.4%; Pred. No. 0; Matches 1464; Conservative 0; Mismatches

DB 3; Length 1870;

| Sequence 15, Appl | Seguence 15, Appl | Sequence 15, Appl | Sequence 15, Appl | Sequence 15, Appl | Sequence 15, Appl | 63 | ę, | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 12, Appl | Sequence 12, Appl | Sequence 12, Appl | Seguence 12, Appl | Seguence 9, Appli |
|---------------------|--------------------|--------------------|---------------------|--------------------|--------------------|---------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|---------------------|---------------------|-------------------|
| 4 US-09-232-149A-15 | 4 US-09-159-812-15 | 4 US-09-636-215-15 | 4 US-09-685-166A-15 | 4 US-09-115-453-15 | 4 US-09-688-489-15 | 4 US-09-312-283C-63 | 3 US-09-188-930-63 | 1 US-07-985-692-1 | 1 US-08-155-331-1 | 1 US-08-424-022-1 | 2 US-08-424-017B-1 | 5 PCT-US93-11696-1 | 1 US-08-155-331-12 | 1 US-08-424-022-12 | 2 US-08-424-017B-12 | S PCT-US93-11696-12 | 1 US-07-972-387-9 |
| 783 4 | 783 4 | 783 | 783 | 783 | 783 | 399 | 399 | 399 | 399 | 399 | 399 | 399 | 3725 | 3725 | 3725 | 3725 | 344 |
| 16.4 | 16 | 16.4 | 16.4 | 16.4 | 16.4 | 11.8 | 11.6 | 4.2 | 4.2 | 4.2 | 5. | 4.2 | 4.2 | 2 | 4 | 5.5 | 3.6 |
| 246.4 | 246 4 | 246.4 | 246.4 | 246.4 | 246.4 | 177 | 174.4 | 62.6 | 62.6 | 62.6 | 62.6 | 62.6 | 62.6 | 62.6 | 62.6 | 62.6 | 53.8 |
| 28 | 00 | í. | | 32 | 33 | 34 | 35 | , es | 37 | 38 | . 6 | 40 | 4.1 | 4 | 43 | 4 4 | 45 |

ALIGNMENTS

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Sequence 6, Application US/99071709
Sequence 7, Application US/99071709
Septicant Hillman, Jennifer L. Applicant East, Freeti
Applicant Hillman, Jennifer L. Applicant Guegler, Rarl J. Applicant Guegler, Marchall, C. Registration Number: Place Guegler, Marchall, Guegler, Gu
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Patent No. 6465622

GENERAL INFORMATION:

APPLICANT: SHIMOMURA, Takeshi
APPLICANT: SHIMOMURA, Toshiya
KITAMURA, Naomi
MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
AND METHOD OF PRODUCING THE PROTEIN
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
MCDIUM TYPE: Floppy Disk
COMFUTER: IBM PC compatible
OOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,449
FILING DATE: 22-Jan-2001
PRIOR APPLICATION NUMBER: 08/685,558
PILING DATE: «Unknown»
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID No: 8
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID No: 8
INFORMATION FOR SEQ ID No: 8
INFORMATION FOR SEQ ID No: 8
ILENGTIAL 1542 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: SUGHRUB, MION, ZINN, MACPEAK
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: no
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1120 CACTGCGTGGACCTGCCAGACACAGGGAGGAGGAGGAGCATCCCGCGCTGGTACTAC 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1300 TTTGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAATGGCTGTGGCA 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1360 Grerrechegrearchecarrengeregragecarchegerrachecrrentaag 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 AGITICCIGGAGIGIGACGACACCCCCAACTGCCCCGACGCCTCCGACGAGGCTGCCTGT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGTCTCCACCAACGACACGAGCACCTGGTCTATAACCACACGACGCGGCCCCTC 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGCGACAAAGGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTITIGAGGAAGAAGAAGAAGTACTCGAGTCTTGTCGCGGCATCTCCCAAGAAGAATGTG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 GGCAGCTCTGGGGCTCAGGCGACTTTCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITGGCCTGAGGCGGGAAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 CACGAGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGTGCTCTGGCACCTGTCAGCCCACCCAGTTCCGCTGCAGCAATGGCTGCTGCATCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                         Length 1542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                 Score 667.4; DB 3;
Pred. No. 3.3e-168;
0; Mismatches 6;
NAME/KEY: signal peptide
LOCATION: 1 to 105
LOCATION: 1 to 105
LOCATION: 1 to 105
LOCATION: 1 to 105
LOCATION: 106
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.1%;
Matches 729; Conservative
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44.3%; Score 667.4; DB 4;
Best Local Similarity 93.1%; Pred. No. 3.3e-168
Matches 729; Conservative 0; Mismatches 6; (ix) FEATURES: SEQUENCE DESCRIPTION: SEQ ID NO: STRAIN: MKN45 US-09-765-449-8 369 1120 쉽 ò

RESULT 3 US-09-765-449-8 ; Sequence 8, Application US/09765449

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US-09-030-607-14/c
US-09-030-607-14/c
Sequence 14, Application US/09030607
Sequence 14, Application US/09030607
Sequence 14, Application US/09030607
Sequence No. 5262245
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS INUMBER OF SEQUENCES: 224
CORRESPONDENCE SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CTIY: Seattle
COUNTRY: USA
ZIP: 98104
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                                                                                    69 TACC-TTCGGGAAGAAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGT-GGGCCTTTGA
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37; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUTCATION INFORMATION:
0; Mismatches
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  459; Conservative
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Patent No. 6261562
CENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                1360 GTGTTCCTGGTCATCFGCATFGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAG 1419
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                                AACCCCTTCAGCGAACACTGCGCCCGCTTTACCTATGGTGGTTGTTACGGCAACAAGAAC 488
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Pred. No. 1.3e-100;
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MEDLIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:

MEDLIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIPICATION:
ATTORNEY/AGRYT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.427C2
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.5%;
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Best Local Similarity
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STATE: WA
COUNTRY: USA
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Alang, Yuqui
APPLICANT: Wi. Jiang, Yuqui
APPLICANT: Wi. Jiang, Yuqui
APPLICANT: Wi. Jiangchui
APPLICANT: Wi. Cham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
TILE REFERENCE: 210121.427CB
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 816
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                                                                                                                                                                                                                                                                   Length 816;
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                                                                                                                                                                                                                                                         Score 413.4; DB 4;
Pred. No. 1.3e-100;
0; Mismatches 37;
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US-09-352-616A-14/C
US-09-352-616A-14/C
; Sequence 14, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
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   ; TYPE: DNA; GRGARISM: Homo sapien; FBATURE: LAME/KEY: misc_feature; LOCATION: (1)...(816); GTHER INFORMATION: n = A,T,C or US-09-439-313-14
                                                                                                                                                                                                                                                            Query Match 27.5%;
Best Local Similarity 92.0%;
Matches 459; Conservative
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ORGANISM: Homo sapien
PRATURE:
NAME/KRY: misc feature
LOCATION: (1)...(816)
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GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Face, Stopen G.
APPLICANT: Red, Michael
APPLICANT: Red, Michael
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Panger, Gary
APPLICANT: Danger, Gary
APPLICANT: Danger, Gary
APPLICANT: Doln, None
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: UNGROUPER: 1999-11-12
CURRENT APPLICATION NUMBER: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE PASSED for Windows Version 3.0
SEQ ID NO 14
LENGTH: 816
                                                                                                                                                                                                                                 Length 816;
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                                                                                                                                                                                                                             27.5%; Score 413.4; DB 3;
92.0%; Pred. No. 1.3e-100;
tive 0; Mismatches 37;
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Patent No. 6329505
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; LENGTH: 816 base pairs; TYPE: nucleic acid STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE: CDNAUS-09-030-607-14
                                                                                                                                                                                                                                                                                           459; Conservative
                                                                                                                                                                                                                                                            Similarity
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patent No. 6613872
GENERAL INPORMATION:
APPLICANT: NI, Jiangchun C.
TITLA OF INVENTION: COMPOUNDS FOR INMUNOTHERAPY OF
TITLE OF INVENTION: COMPOUNDS FOR INMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C5
CURRENT PRILIG DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE PASISE FASTSEQ for Windows Version 3.0
SEQ ID NO 14
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 816;
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Best Local Similarity 92.0%; Pred. No. 1.3e-100;
Matches 459; Conservative 0; Mismatches 37;
9 CACCAGGAGCAGATCTGCAAGAGTTTCGTT
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NAME/KEY: misc feature
LOCATION: (1)...(816)
CTHER INFORMATION: n = A,F,C or G
US-09-159-812-14
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ORGANISM: Homo sapien
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                                                     Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
ITILE OF INVENTION: COMPOUNDS FOR INMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121.42766
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ IO NOS: 338
SOFTWARE: FASTERQ for Windows Version 3.0
                                                                                       Indels
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                                                       Score 413.4; DB 4;
Pred. No. 1.3e-100;
0; Mismatches 37;
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US-09-232-149A-14/c
* Sequence 14, Application US/09232149A
; Patent No. 6465611
   // OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-14
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NAME/KEY: misc feature

LOCATION: (1)...(816)

OTHER INFORMATION: n = A,T,C or
US-09-232-149A-14
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Best Local Similarity 92.0%;
Matches 459; Conservative
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ORGANISM: Homo sapien
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LENGTH: 816
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hebber, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SEQ ID NO : 898
SEQ ID NO : 898
SEQ ID NO 14
IRNGTH: 816
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; Sequence 14, Application US/09685166A
; Patent No. 6530305
; GENERAL INFORMATION:
; APPLICANT: XL, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.42777C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID MOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 14, Application US/09636215
; Patent No. 6620922
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OTHER INFORMATION: n = A,T,C or G
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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ORGANISM: Homo sapien
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APPLICANT: Xu, Jian
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LENGTH: 816
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TYPE: DNA
ORGANISM: Homo sapien
FRATURE:
NAPME/KEY: misc_feature
LOCATION: (1)...(816)
OTHER INFORMATION: n = A,T,C or

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198 CCCNCGGAGCAGAINTGCAAGAGTTT-GTTTANGGGGNTGGNTTGGGCAACAAGAANAAC 440
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Sequence 14, Application US/09689489

Sequence 14, Application US/09689489

Setent No. 6664377

GENERAL INFORMATION:

APPLICANT: Willon, Davin C.

APPLICANT: Mitcham, Jennifer Lynn

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

TITLE REFERENCE: 210121.427D2

CURRENT FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 216
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27.5%; Score 413.4; DB 4;
Best Local Similarity 92.0%; Pred. No. 1.3e-100;
Matches 459; Conservative 0; Mismatches 37;
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COTHER INFORMATION: n = A,T,C or G
US-09-688-489-14
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NAME/KEY: misc_feature
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ORGANISM: Homo sapien
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US-09-115-433-14/C
US-09-115-433-14/C
Sequence 14, Application US/09115453B
Patent No. 6657056
GENERAL INFORMATION:
APPLICANT XU, Jiangchun
APPLICANT XU, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C4
CURRENT TRIING DATE: 1998-07-14
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PASISEQ for Windows Version 3.0
SOFTWARE: RASISEQ for Windows version 3.0
TYPE: DNA
COMPANIEM: 816
TYPE: DNA
COMPANIEM: 816
COMPAN
                                                                                                                                                                                                                                                                                                                                      498 cccncccaccacatriccaacatri-critangscentecritccccaacaanaac 440
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                                                                                                    Length 816;
                                                                                                                                                                             Indels
                                                                                           27.5%; Score 413.4; DB 4;
92.0%; Pred. No. 1.3e-100;
ive 0; Mismatches 37;
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459; Conservative
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NAME/KEY: misc feature
LOCATION: (1)...(816)
OTHER INFORMATION: n =
                 US-09-685-166A-14
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Best Local S:
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127 GAGGCAGCTCTGGGGCTCAGGCGACTTTCCCCCCAGGGCCCCTCCATGGAAAGGCGCCATC 186

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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS I
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
                                                  416 TICTAGCCTGTCGGGGTGTGCAAGGT-GGCCTTTGAGAGGCAGTTTGGG----NTNAGGN 362
                                                                                                                                                                                                                                                                    151 CTTTCCCCCAGGGCCCTCCATGGAAAGGCGCCATCCAGTGTGTCTCTGGCACCTGTCAGC 210
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                                                                                                                                                                                                                                                                                                                   361 GATTICCCCCAGGCCCTTCCATGGAAAGGC-CNATCCAGTGTGTTCTGGCACCTGTCAGC 303
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WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILLING DATE: 25-FRB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/09030607
Patent No. 6262245
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NAME: Maki, David J.
REGIGSTRATTON UNDER: 21012
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INPORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 632-6031
INPORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-020-956-37/c
is Sequence 37, Application US/09020956
is Datent No. 6261562
is GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
ITILE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
ITILE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
INDMESSEE: 178
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         199 GIGAAAAAITACACGAGTGGCTTTGACGAGGTCCAGTGCCATTTCCCCAGTGACAAAG 140
                                                                                                         187 CAGTGTGCTCTGGCACCTGTCAGCCCAGTTCCGCTGCAGCAATGGCTGCTGCATCG 246
                                                                                                                                                                                                                                                                                      259 ACAGTITCCTGGAGTGTGAGAGACCCCCAACTGCCCCGACGCGCGACGAGGCTGCCT 200
GAGGCAGNTNTGGGGNTCAGGGACTTTCCCNCAGGGCCCNTNNCATGGAAAGGCGCCATC 320
                                                                                                                                                                      319 cadróricororidecamiencadocoadocadrirocoriscadoaaridecidoridoanid 260
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-PEB-1998
CLASSIFICATION:
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NAME: Waki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMULCATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 632-6931
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 90.2
Matches 432; Conservative
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MOLECULE TYPE:
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COUNTRY:
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242 ACCCCCAACTGCCCGGANGCTTCGGAGGAGGAGGCTGCNTGTGAAAAATACACGAGTGGNTTN 183
                                                                                 476 TIGGITIGNIGGAGGNIGCITGGGAACAACAACTACCTITGGGAAGAAGAGAGGAI 417
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                                                        32 TITCGITIATGGAGGCTGCTTGGGCAACAAGAACAACTACCTTCGGGAAGAAGAAGAGCA- 90
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23.8%; Score 357.8; DB 3; Length 760; 90.2%; Pred. No. 8.4e-86; ive 0; Mismatches 39; Indels B
Query Match
Best Local Similarity 90.2
Matches 432; Conservative
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Search completed: April 22, 2004, 08:12:04 Job time : 125 secs

Sequence Seq

US-08-398-010A-57 US-08-398-010A-59 US-08-398-010A-62 US-08-398-010A-65 US-08-398-010A-67 US-08-398-010A-67 US-08-398-010A-68 US-08-398-010A-69 US-08-398-628A-33 US-08-398-628A-53 US-08-398-628A-53 US-08-398-628A-54 US-08-398-628A-54 US-08-398-628A-54 US-08-398-628A-54 US-08-398-628A-54 US-08-398-628A-54 US-08-398-628A-54 US-08-398-628A-59 US-08-398-628A-59 US-08-398-628A-59 US-08-398-628A-59 US-08-398-628A-59 US-08-398-628A-59 US-08-398-628A-59

Sequence

ALIGNMENTS

RESULT 1 US-09-071-709-2 Sequence 2, Appli Sequence 18, Appl Sequence 182, Appl Sequence 182, App Patent No. 5208144 Sequence 2, Appli April 22, 2004; 10:22:35; Search time 23 Seconds (without alignments) 462.389 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description US-09-935-390A-23 206 1 MERRHPVCSGTCQPTQFRCS.....TVSTTEDTEHLVYNHTFRPL Issued Patents AA:*

(/GGTZ 6/ptodate/2/iaa/5A_COMB.pep:*

(/GGTZ 6/ptodate/2/iaa/5B_COMB.pep:*

(/GGTZ 6/ptodate/2/iaa/6A_COMB.pep:*

(/GGTZ 6/ptodate/2/iaa/6B_COMB.pep:*

(/GGTZ 6/ptodate/2/iaa/PGTUS_COMB.pep:*

(/GGTZ 6/ptodate/2/iaa/PGTUS_COMB.pep:*

(/GGTZ 6/ptodate/2/iaa/PGTUS_COMB.pep:* GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. US-09-071-709-2 US-09-685-558A-18 US-09-312-283C-182 US-09-312-283C-182 S208.144-20 5208.144-20 US-09-040-774-2 US-08-566-800A-32 US-08-566-800A-32 US-08-566-800A-47 US-08-566-800A-47 US-08-566-800A-47 US-08-566-800A-47 US-08-566-800A-52 US-08-566-800A-51 US-08-566-800A-53 US-08-566-800A-53 US-08-566-800A-53 US-08-566-800A-53 US-08-566-800A-53 US-08-566-800A-53 US-08-566-800A-53 US-08-566-800A-53 US-08-566-800A-54 US-08-566-800A-54 US-08-566-800A-54 US-08-566-800A-54 US-08-566-800A-54 US-08-398-90-33 US-08-398-90-33 US-08-398-90-33 US-08-398-90-33 US-08-398-90-33 Total number of hits satisfying chosen parameters: 389414 segs, 51625971 residues SUMMARIES Post-processing: Listing first 45 summaries OM protein - protein search, using sw model OLIGO Gapop 60.0 , Gapext 60.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Query Match Length Title: Perfect score: Scoring table: Word size : Database : Sequence:

GENURAL INFORMATION:
GENURAL INFORMATION:
GENURAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Inal, Preeti
APPLICANT: Corley, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN PROFEASE ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTER PHARMACEUTICALS, INC. COMPUTER REALBABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
FOLOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Herewith
APPLICATION DATA:
FILING DATE: Filed Herewith
CLASSIFICATION:
MANE: CERCONS, MICHAEL C.
REGISTRATION NUMBER: 39,132
FEREPREMOR/DOCKEY NUMBER: 99,132
FELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single 12
12
12
13
14 PORTER PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304 IMMEDIATE SOURCE: LIBRARY: BLADNOT04 CLONE: 1319265 CLONE: CLONE: US-09-071-709-2

Sequence 32,

Result No.

Sequence Sequence Sequence

Gaps ö Indels 100.0%; Score 206; DB 3; L ilarity 100.0%; Pred. No. 1.1e-187; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 206; Conserv

Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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428 ISKKDVFGLRREIPIPSTGSVEWAVAVELVICIVVVVVALLGYCFFKNQRKDFHGHHPPP 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ISKKDVFGLRREIPIPSTGSVEMAVAVFLVICIVVVVAILGYCPFKNORKDFHGHHHHPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428 ISKKDVPGLRREIPIPSTGSVEMAVAVFLVICIVVVVALIGYCFFKNQRKDFHGHFHPP 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MERRHPVCSGTCQPFQFRCSNGCCIDSFLECDDTPNCPDASDBAACEKYTSGFDELQRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 206; DB 4; Length 513; 100.0%; Pred. No. 1.5e-187; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       KITAMURA, Naomi
MIYAZAWA, Kelji
TITLE OF INVENTION: NORLSIN, DNA CODING FOR SAME
AND METHOD OF PRODUCING THE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER IBM PC compatible
COMPUTE: BM PC compatible
COMPUTE: BM PC compatible
COMPUTE: BM PC compatible
COPERATING SYSTEM: PO-DCS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,449
FILING DATE: 2-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERESTICS:
SEQUENCE CHARACTERESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STRET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: MKW45
SEQUENCE DESCRIPTION: SEQ ID NO: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTPASSTVSTTEDTEHLVYNHTTRPL 513
                                                                         181 PTPASSTVSTTEDTEHLUYNHTTRPL 206
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                                                                                                                 488 PTPASSIVSTIEDIEHLVYNHITRPL
                                                                                                                                                                                                                           Sequence 18, Application US/09765449
Patent No. 6465622
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               APPLICANT: SHIMOMURA, Takeshi
KAWAGUCHI, Toshiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity 100.
206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                        US-09-765-449-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-765-449-18
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Best Local S
Matches 206
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                                                                                                                                          PSDKGHCVDLPDTGLCKESIPRMYNPFSEHCARFIYGGCYGNKNNFEEQQCLESCRG 262
                                                                                                                                                                                                        ISKKDVFGLRREIPIPSTGSVEMAVAVFLVICIVVVVAILGYCFFKNQRKDFHGHHHHPP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427
                                                        143 MERRHPVCSGTCQPTQPRCSNGCCIDSFLECDDTPNCPDASDEAACEKYTSGFDELQRIH 202
                                                                                                                   PPSDKGHCVDLPDTGLCKBSIPRWYYNPFSEHCARFTYGGCYGNKNNFBEBQQCLBSCRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNNFEEBQQCLESCRG 120
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APPLICANT: KHMOMUTA, Takeshi
APPLICANT: KHMOMUTA, Takeshi
APPLICANT: MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
TITLE OF INVENTION: NOVEL PROTEIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,558A
FILING DATE: 24-JUL-1996
PRIOR APPLICATION NUMBER: US Hei 7-187135
FILING DATE: 24-JUL-1995
INPORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 206; DB 3; L 100.0%; Pred. No. 1.5e-187; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                    PIPASSIVSTIBDIEHLVYNHITRPL 348
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MKN45
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
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ORIGINAL SOURCE:
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Best Local
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Query Match
Best Local Similarity
Matches 11; Conserva
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LENGIH: 726
                                                                                                                                                                                                           SEQ ID NO:20:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-040-774-2
                                                                                                                                                                                                                                                         5208144-20
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,Patent No. 5208144
,APPLICANT: SMITH, JOHN A.,RAYCHOWDHURY, RAKTIMA;NILES, JOHN L. TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA;CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
US-09-312-283C-182

| Sequence 182, Application US/09312283C|
| Patent No. 6573095|
| GENERAL INFORMATION:
| APPLICANT: Watson, James D. |
| APPLICANT: Steachan, Lorna |
| APPLICANT: Steachan, Matthew |
| APPLICANT: Steachan, Matthew |
| APPLICANT: Gurust, Rene |
| APPLICANT: Kumble, Krishanand D. |
| TITLE OF INVENTION: Compositions Isolated from Skin Cells |
| TITLE OF INVENTION: and Methods for Their Use |
| FILE REPERENCE: 11000.1011c2 |
| CURRENT APPLICATION NUMBER: US/09/312,283C |
| CURRENT FILING DAIE: 1999-05-14 |
| NUMBER OF SEQ ID NOS: 425 |
| SOFTWARE: FRSEESEQ for Windows Version 4.0 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 182. Application US/09188930A

Patent No. 6150502

GRAKEAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Streachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Ornurat, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methode For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT PILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOUTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 182
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.1%; Score 27; DB 4; Length 72; 100.0%; Pred. No. 2.6e-18; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%; Score 21; DB 3; Length 72; 100.0%; Pred. No. 1.3e-12; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 27, Conservative
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Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mouse
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ORGANISM: mouse
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US-09-188-930-182
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APPLICART: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.
TITLE OF INVENTION: WETHOD FOR DETECTION OF HUMAN DNA
CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
NUMBER OF SEQUENCES: 42
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATE: US/07/396,697
FILING DATE: 22-ADG-1989
FILING DATE: 22-FDE-1989
FILING DATE: 22-FDE-1989
FILING DATE: 22-FDE-1989
FILING DATE: 23-FDE-1989
FILING DATE: 23-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.3%; Score 11; DB 6; Length 726;
00.0%; Pred. No. 0.025;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             5.3%; Score 11; DB 6; Length 38;
100.0%; Pred. No. 0.0024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Trygrason, Karl
APPLICANT: Kestila, Marjo
APPLICANT: Lenkeri, Ulla
APPLICANT: Lenkeri, Ulla
APPLICANT: Mannikko, Minna
ITILE OF INVENTION: Nephrin Gene and Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSED MCDonnell Boehnen Hulbert & Bergho
STREET: 300 S. Wacker Drive, Suite 3200
CITY: Chicago
STATE: 11
                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/396,697
FILING DATE: 22-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 313,682
FILING DATE: 22-FEB-1989
APPLICATION NUMBER: 235,211
FILING DATE: 23-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
SOPTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09040774 Patent No. 6207811
                                                                                                                                                                                                                                                                                                                                                             11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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LENGTH: 58 amino acids
TYPE: Amino Acid
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Best Local Similarity 100.
Matches 7; Conservative
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COMPUTER READABLE FORM:
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                                                                                  35 YGGCYGN 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 YGGCYCN 41
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| Sequence 32, Application US/08566800A
| Sequence 32, Application US/08566800A
| Patent No. 5736364
| Patent No. 5736364|
| APPLICANT: Kalley, Robert F. APPLICANT: Lazarus, Robert A. APPLICANT: Lee, Geoffrey F. TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors NUMBER OF SEQUENCES: 58
| CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. STREET: ADDRESSE: Genentech, Inc. STREET: South San Francisco CITY: South San Francisco STREET: ADDRESSE: Genentech, Inc. STREET: ADDRESSE: Genentech, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1241;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM:
OPERATING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIPICATION: 514
ATTORNEY/AGBNT INFORMATION:
NAME: KUDINGC, JGFfrey S.
REGISTRATION NUMBER: 36,575
REGISTRATION STATE JGFTERS: 190,531-7168
INFORMATION FOR SEQ ID NO: 32:
SEQUENT: GRARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.9%; Score 8; DB 3
100.0%; Pred. No. 27;
tive 0; Mismatches
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100.0%; Pred. No. 21;
tive 0; Mismatches
                                     APPLICATION NUMBER: US/09/040,774
FILING DATE: 18 MAR 1998
CLASSIFFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 97,842
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1241 amino acids
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-040-774-2
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Gaps
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RESULT 10
US-08-566-800A-37
US-08-56-800A-37
Sequence 37, Application US/0856800A
Patent No. 5736364
GENERAL INFORMATION:
APPLICANT: Kelley, Robert P.
APPLICANT: Lee, Geoffrey P.
APPLICANT: Lee, Geoffrey P.
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetech, Inc.
STREET: 460 Point San Bruno Blvd
COUNTRY: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-566-800A-38
Sequence 38, Application US/0856800A
SEQUENCE 30, Robert F.
APPLICANT: Lazarus, Robert F.
APPLICANT: Lazarus, Robert A.
SEQUENCES: 58
CORRESOUNDENCES: 58
CORRESOUNDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STRTE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 37:
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; Sequence 44, Application US/08566800A
; Sequence 44, Application US/08566800A
; GENERAL INFORMATION:
    APPLICANT: Melley, Robert A.
    APPLICANT: Lazarus, Robert A.
    APPLICANT: Lee, Geoffrey F.
    TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
    TITLE OF INVENTION: So
    CORRESPONDENCE: 58
    CORRESPONDENCE: Genencech, Inc.
    ADDEESSER: Genencech, Inc.
    ASTREET: 460 Point San Bruno Blvd
    CITY: South San Francisco
                                                                                                                                                                                                                                    US-08-566-800A-42

US-08-566-800A-42

Sequence 42, Application US/08566800A

Patent No. 5736364

GRNERAL INFORMATION:
APPLICANT: Lazarus, Robert A.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: No. 5736364el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
ADDRESSEE: 460 Foint San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.4%; Score 7; DB 1; Length 58; 100.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
  Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY: USA
ZIP: 94080
COMPUTER READABLE PORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARTS: Winbatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 5.14
ATYONEY/AGENT INPORMATION:
REFERENCE/DOCKET NUMBER: 96.575
RECTORMUTCATION NINPERR: 96.575
REFERENCE/DOCKET NUMBER: 90.958B
TELECOMMUTCATION INFORMATION:
TELEPRONE: 415/225-928
TELEPRONE: 415/225-928
TELEPRONE: 415/225-9828
TELEPRONE: 415/225-928
TELEPRONE: 415/225-928
TELEPRONE: 415/225-928
TELEPRONE: 415/225-928
    3.4%; Score 7; DB 1;
100.0%; Pred. No. 21;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 940°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 amino acids
                           Best Local Similarity 100. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100 Matches 7; Conservative
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                                                                                                   98 YGGCYGN 104
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         Query Match
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US-08-56-8004-39

Patent No. 5736364

GENERAL INFORMATION:
APPLICANT: Lazarus, Robert F.
APPLICANT: Lazarus, Robert F.
APPLICANT: Lazarus, Robert A.
APPLICANT: California
COUNTRY: South San Francisco
STATE: California
COUNTRY: USA
COMPUTER: Lazarus Form:
APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
ATTORNEY/ARENT INFORMATION:
APPLICATION NUMBER: 36,575
REGISTRATION NUMBER: 36,575
TELEPAN: 415/522-8981
TELEPAN: 415/522-8981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 58;
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech) CURRENT APPLICATION DATA: US/08/56,800A FPLICATION NUMBER: US/08/56,800A FILING DATE: 04-Dec-1995 CLASSIFICATION: 514 ATTORNEY/AGENT INPORMATION: NAME: Kubinec, Jeffrey S. REGISTRATION NUMBER: 36,575 REGISTRATION NUMBER: 36,575 TELECOMMUNICATION: TELEFAX: 415/52-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4%; Score 7; DB 1
100.0%; Pred. No. 21;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: 58 amino acids
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INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 58 amino acids
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
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US-08-566-800A-39
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Search completed: April 22, 2004, 10:26:18
Job time : 24 secs
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                      , TOPOLOGY: Linear
US-08-566-800A-45
TYPE: Amino Acid
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US-08-566-800A-45
IS-66-800A-45
Sequence 45. Application US/08566800A
Patent No. 573634
GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
COUNTRY: USA
ZIP: 94080
COUNTRY: USA
ZIP: 94080
COMPUTER READALE FORM:
MEDIUM TYPE: 3 5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC-COS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION NUMBER: 96/565,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION NUMBER: 109/08/56
FILING DATE: 04-Dec-1995
CLASSIFICATION NUMBER: P0958B
TELERAX: 415/252-982B
TELERAX: 415/252-982B
TELERAX: 415/252-982B
TELERAX: 415/252-983
INFORMATION FOR SEQ IN NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 58; . 21;
                 COUNTRY: USAN
ZIP: 94060
COMPUTER READBALE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 %D floppy disk
COMPUTER: IBM PC compatible
ODREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REGISTRATION NUMBER: 36,575
RECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9828
TELEPHONE: 415/952-9828
TELEPHONE: 415/952-9828
TELEPHONE: 415/952-9828
TELEPHONE: 415/952-9828
TELEPHONE: 415/952-9828
TELEPHONE: AND ONE 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.4%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
California
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Gaps
                            ö
                            0; Indels
 Length 58;
3.4%; Score 7; DB 1;
100.0%; Pred. No. 21;
cive 0; Mismatches
 Query Match
Best Local Similarity 100.
Matches 7; Conservative
```

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